

Nashed
Seg. 1 of 2
w/ interf

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:17:29 : Search time 3114 Seconds
(without alignments)
4093.526 Million cell updates/sec

Title: US-09-975-456B-1
Perfect score: 507
Sequence: 1 atgaagaagttcttcacagt.....cgccccccgccccctccctag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 85: /cgn2_6/ptodata/2/pna/US6041_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	100.0	507	US-09-975-456B-1	Sequence 1, Appl
2	507	100.0	2270	US-60-203-511-4	Sequence 4, Appl
3	507	100.0	2270	US-60-403-468-3	Sequence 3, Appl
4	505.4	99.7	2716	US-10-104-047-1765	Sequence 1765, Ap
5	464	91.5	748	US-60-212-356-317	Sequence 317, App
6	464	91.5	829	US-60-212-356-282	Sequence 282, App
7	379	74.8	379	US-60-229-525-741	Sequence 741, App
8	342.2	67.5	903	US-60-360-207-10397	Sequence 10397, A
9	305	60.2	748	US-60-229-525-724	Sequence 724, App
10	252.4	49.8	748	US-60-229-525-571	Sequence 571, App
11	240	47.3	256	US-60-234-446-1225	Sequence 1225, Ap
12	222.8	43.9	483	US-60-126-590-447	Sequence 447, App
13	212	41.8	627	US-60-160-203-829	Sequence 829, App
14	212	41.8	4179	US-60-207-316-43	Sequence 43, Appl
15	199.4	39.3	1644	US-09-609-137-56	Sequence 56, Appl
16	199.4	39.3	1644	US-10-137-659-56	Sequence 56, Appl
17	167.2	33.0	388	US-10-137-659-38	Sequence 38, Appl
18	167.2	33.0	388	US-10-137-659-38	Sequence 103, App
19	126	24.9	549	US-60-196-174-103	Sequence 686, App
20	115	22.7	712	US-60-177-571-686	Sequence 15647, A
21	110.8	21.9	560	US-09-634-306B-15647	

c 22 110.8 21.9 560 38 US-10-027-632-15647 Sequence 15647, A
 23 100.6 19.8 549 17 US-09-362-510-22948 Sequence 22948, A
 24 100.6 19.8 549 17 US-09-362-510-22948 Sequence 22948, A
 25 100.6 19.8 549 17 US-09-489-036-8343 Sequence 8343, A
 26 100.6 19.8 549 34 US-09-904-013-22948 Sequence 22948, A
 27 100.6 19.8 549 35 US-09-943-143-8343 Sequence 8343, A
 28 99.4 19.6 674 19 US-09-528-409-31852 Sequence 31852, A
 29 99.4 19.6 674 35 US-09-933-524-31852 Sequence 31852, A
 30 99.4 19.6 674 35 US-09-933-524-31852 Sequence 31852, A
 31 99 19.5 451 19 US-09-528-409-70519 Sequence 70519, A
 32 99 19.5 451 35 US-09-933-524-70519 Sequence 70519, A
 33 99 19.5 451 35 US-09-933-524-70519 Sequence 70519, A
 34 99 19.5 476 18 US-09-489-036-30282 Sequence 30282, A
 35 99 19.5 476 35 US-09-943-143-30282 Sequence 30282, A
 36 99 19.5 592 15 US-09-181-317-3 Sequence 3, Appli
 37 99 19.5 719 35 US-09-528-409-68551 Sequence 68551, A
 38 99 19.5 719 35 US-09-933-524-68551 Sequence 68551, A
 39 99 19.5 854 1 PCT-US01-10542-6 Sequence 6, Appli
 40 99 19.5 854 36 US-09-969-384-6 Sequence 26, Appli
 41 99 19.5 878 32 US-09-856-486-26 Sequence 281, Appli
 42 99 19.5 901 65 US-09-347-127-91 Sequence 91, Appli
 43 99 19.5 1687 17 US-09-905-059-91 Sequence 91, Appli
 44 99 19.5 1687 34 US-09-905-059-91 Sequence 91, Appli
 45 99 19.5 1687 34 US-09-905-059-91 Sequence 91, Appli

ALIGNMENTS

RESULT 1
 ; Sequence 1, Application US/09975456B
 ; GENERAL INFORMATION:
 ; APPLICANT: LAZDUNSKI, MICHEL
 ; APPLICANT: LAMBEAU, GERARD
 ; APPLICANT: VALENTIN, EMMANUEL
 ; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
 ; FILE REFERENCE: 1478-R-00
 ; CURRENT APPLICATION NUMBER: US/09/975,456B
 ; PRIOR FILING DATE: 2002-08-27
 ; PRIOR APPLICATION NUMBER: 60/239,491
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 2.1
 ; SEQ ID NO 1
 ; LENGTH: 507
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(507)
 ; OTHER INFORMATION: cdna encoding human group IIF secreted phospholipase A2
 US-09-975-456B-1

Query Match
 Best Local Similarity 100.0%; Score 507; DB 36; Length 507;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAAGAAGTCTTCAACCTGGCCATCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
 Db 1 ATGAAGAAGTCTTCAACCTGGCCATCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
 Qy 61 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCGCTACAGGAGGAGGAGCGCCATCCTGTCC 120
 Db 61 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCGCTACAGGAGGAGGAGCGCCATCCTGTCC 120
 Qy 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCGCGTGGCCAGCCCAAGGATGAGGTG 180
 Db 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCGCGTGGCCAGCCCAAGGATGAGGTG 180
 Qy 181 GACTGGTGCTGCCAGGCCACGACTGCTGTACCAAGAACTCTTTACCAAGGCTGTAC 240
 Db 181 GACTGGTGCTGCCAGGCCACGACTGCTGTACCAAGAACTCTTTACCAAGGCTGTAC 240

Qy 241 CCTATGTGGACCATATGATCACACCATCGAGAAACACACTGAGATAGTCTGCAGTGAC 300
 Db 241 CCTATGTGGACCATATGATCACACCATCGAGAAACACACTGAGATAGTCTGCAGTGAC 300
 Qy 301 CTCAACAAGACAGAGTGTGACAAGCAGACATGCGATGTGTGACAAGAAACATGGTTCGTGTC 360
 Db 301 CTCAACAAGACAGAGTGTGACAAGCAGACATGCGATGTGTGACAAGAAACATGGTTCGTGTC 360
 Qy 361 CTCATGAACCAAGAGCTTACCGAGAGAGTACCGTGGCTTCCTCAATGCTACTGCCAGGGC 420
 Db 361 CTCATGAACCAAGAGCTTACCGAGAGAGTACCGTGGCTTCCTCAATGCTACTGCCAGGGC 420
 Qy 421 CCACAGCCCAACTGCAGCATCTATGAACCGCCCTTGAGGAGGTCACTGCACTGACCA 480
 Db 421 CCACAGCCCAACTGCAGCATCTATGAACCGCCCTTGAGGAGGTCACTGCACTGACCA 480
 Qy 481 TCCCAAGCCCGCCCGCCCTCCCTAG 507
 Db 481 TCCCAAGCCCGCCCGCCCTCCCTAG 507

RESULT 2

US-60-203-511-4
 ; Sequence 4, Application US/60203511
 ; GENERAL INFORMATION:
 ; APPLICANT: Das, Debopriya
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Yao, Monique G.
 ; APPLICANT: Nguyen, Dannel B.
 ; APPLICANT: Lu, Yan
 ; APPLICANT: Tribouley, Catherine M.
 ; APPLICANT: Yue, Henry
 ; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
 ; FILE REFERENCE: PI-0095 P
 ; CURRENT APPLICATION NUMBER: US/60/203,511
 ; CURRENT FILING DATE: 2000-05-11
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 4
 ; LENGTH: 2270
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; OTHER INFORMATION: Incyte ID No: 7473224CB1
 US-60-203-511-4

Query Match
 Best Local Similarity 100.0%; Score 507; DB 64; Length 2270;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAAGAAGTCTTCAACCGTGGCCATCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
 Db 222 ATGAAGAAGTCTTCAACCGTGGCCATCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
 Qy 61 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCGCTACAGGAGGAGGAGCGCCATCCTGTCC 281
 Db 282 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCGCTACAGGAGGAGGAGCGCCATCCTGTCC 281
 Qy 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCGCGTGGCCAGCCCAAGGATGAGGTG 341
 Db 342 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCGCGTGGCCAGCCCAAGGATGAGGTG 341
 Qy 181 GACTGGTGCTGCCAGGCCACGACTGCTGTACCAAGAACTCTTTACCAAGGCTGTAC 401
 Db 402 GACTGGTGCTGCCAGGCCACGACTGCTGTACCAAGAACTCTTTACCAAGGCTGTAC 401
 Qy 241 CCTATGTGGACCATATGATCACACCATCGAGAAACACACTGAGATAGTCTGCAGTGAC 461
 Db 462 CCTATGTGGACCATATGATCACACCATCGAGAAACACACTGAGATAGTCTGCAGTGAC 461


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; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-356-317

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Query Match 91.5%; Score 464; DB 65; Length 748;
Best Local Similarity 100.0%; Pred. No. 5,8e-105;
Matches 464; Conservative 0; Mismatches 0; Indels

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QY	1	ATGAGAAGTTCTTACCGTGGCCATCCTTGTCGACGTTCTGTCCACAGCTCAGCGC	60
Db	131	ATGAAGAAGTTCTTACCGTGGCCATCCTTGTCGACGTTCTGTCCACAGCTCAGCGC	190
QY	61	AGCCTGCTCAACCTGAAGCCCATGTGAGGCCGTACAGGAGGAGCGCATCTCTGTCC	120
Db	191	AGCCTGCTCAACCTGAAGCCCATGTGAGGCCGTACAGGAGGAGCGCATCTCTGTCC	250
QY	121	TTGCTGGGCTACGGTTGCTACTGTGGGTGGGGGGCGTGGCCAGGCCCAAGGATGAGGTG	180
Db	251	TTGCTGGGCTACGGTTGCTACTGTGGGTGGGGGGCGTGGCCAGGCCCAAGGATGAGGTG	310
QY	181	GACTGTGTCTGCACGCCCCAGCTGCTGTCTACAGGAACCTTTGACCAAGGCTGTCAAC	240
Db	311	GACTGTGTCTGCACGCCCCAGCTGCTGTCTACAGGAACCTTTGACCAAGGCTGTCAAC	370
QY	241	CCCTATGTGGACCACTATGATCACACCATCGAACAACACTGAGATAGTCTGCAAGTAC	300
Db	371	CCCTATGTGGACCACTATGATCACACCATCGAACAACACTGAGATAGTCTGCAAGTAC	430
QY	301	CTCAACAAGACAGAGTGTGACACGACACATGATGTGTGACAAGAACAATGTTCTGTGC	360
Db	431	CTCAACAAGACAGAGTGTGACACGACACATGATGTGTGACAAGAACAATGTTCTGTGC	490
QY	361	CTCATGAACCAAGCGTACCAGAGGAGTACCGTGGCTTCCTCAAGTGTCTACTGCCAGGC	420
Db	491	CTCATGAACCAAGCGTACCAGAGGAGTACCGTGGCTTCCTCAAGTGTCTACTGCCAGGC	550
QY	421	CCCAAGGCCCAACTGCAAGCTATGAACCGCCCGCTGAGAGGT	464
Db	551	CCCAAGGCCCAACTGCAAGCTATGAACCGCCCGCTGAGAGGT	594

RESULT 6

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US-60-212-356-282
; Sequence 282, Application US/60212356
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000677
; CURRENT APPLICATION NUMBER: US/60/212,356
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 829
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-356-282

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Query Match	91.5%	Score 464;	DB 55;	Length 829;
Best Local Similarity	100.0%;	Pred. No. 5.9e-105;		
Matches 464;	Conservative	0;	Mismatches 0;	Indels

0

QY 1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGTGGCAGCGTCTGTCCACAGGTCACGGC 60
|||||
Db 131 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGTGGCAGCGTCTGTCCACAGGTCACGGC 190

Qy	61	AGCCTGCTCAACCTGAAGGCCATGTGGAGCCGTACACGGAGGAGCGCCATCCTGTCC	120
Db	191	AGCCTGCTCAACCTGAAGGCCATGGTGGAGCCGTACAGGGAGGAGCGCCATCCTGTCC	250
Qy	121	TTCTGGGCTAGGTTTGTACTGTGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG	180
Db	251	TTCTGGGCTACGTTTGTACTGTGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG	310
Qy	181	GACTGGTCTGCCACGCCACGACTGCTGTACTACGAGAACTCTTTGACCAAGCTGTCAAC	240
Db	311	GACTGGTCTGCCACGCCACGACTGCTGTACTACGAGAACTCTTTGACCAAGCTGTCAAC	370
Qy	241	CCCTATGTGGACCACTATGATCACACCATCGAGAAACAACACTGAGATAGCTGCAAGTAC	300
Db	371	CCCTATGTGGACCACTATGATCACACCATCGAGAAACAACACTGAGATAGCTGCAAGTAC	430
Qy	301	CTCAACAAGACAGAGTGTGACAGCAGACATGCATGTGTGACAAGAACATGTTCTGTGC	360
Db	431	CTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAAGAACATGTTCTGTGC	490
Qy	361	CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCTCTCAATGTCTACTGCCAGGC	420
Db	491	CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCTCTCAATGTCTACTGCCAGGC	550
Qy	421	CCACGCCCAACTGCAGCATCTATGAACCGCCCTCGAGGAGT	464
Db	551	CCACGCCCAACTGCAGCATCTATGAACCGCCCTCGAGGAGT	594

RESULT 7

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US-60-229-525-741
; Sequence 741, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 741
; LENGTH: 379
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-741

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Query Match

Query Match 74.8%; Score 379; DB 66; Length 379;
 Best Local Similarity 100.0%; Pred. No. 7.1e-84;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	57	CGCGCGCTGCTCAACCTGAAGGCCATGTGTGAGGCCGTACAGAGGAGGAGCGCCATCCT	116
Db	1	CGCGCGCTGCTCAACCTGAAGGCCATGTGTGAGGCCGTACAGAGGAGGAGCGCCATCCT	60
QY	117	GTCTTTCGTGGGCTACGGTTGCTACTGTGGGTGGGGGCCGTGGCCAGGCCAAGGATGA	176
Db	61	GTCTTTCGTGGGCTACGGTTGCTACTGTGGGTGGGGGCCGTGGCCAGGCCAAGGATGA	120
QY	177	GTGTGACTGTGTCTGCCACGCCACGACTGTCTGTACCAGGAACCTCTTTGACCAAGCGTG	236
Db	121	GTGTGACTGTGTCTGCCACGCCACGACTGTCTGTACCAGGAACCTCTTTGACCAAGCGTG	180
QY	237	TCACCCCTATGTGGACCACTATGATCACACCATCCAGAAACAACACTCAGATAGTCTGGAG	296
Db	181	TCACCCCTATGTGGACCACTATGATCACACCATCCAGAAACAACACTCAGATAGTCTGGAG	240
QY	297	TGACCTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAGAACATGTTCT	356
Db	241	TGACCTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAAGAACATGTTCT	300
QY	357	GTGGCTCATGAACCAAGCTACCGAGAGGATACCGTGGCTCTCTCAATCTCTACTCGCA	416


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Db 301 GTGCTCATGAACACAGAGTACCGAGAGGAGTACCGTGGCTTCTCAATGCTACTGCCA 360
Qy 417 GGGCCCCACGCCCACTGC 435
Db 361 GGGCCCCACGCCCACTGC 379

RESULT 8
US-60-360-207-10397
; Sequence 10397, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 10397
; LENGTH: 903
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-10397
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Query Match 67.5%; Score 342.2; DB 80; Length 903;
Best Local Similarity 79.7%; Pred. No. 1.2e-74;
Matches 404; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 1 ATGAAGAAGTCTTTCACCGTGGCCATCTTGCTGGCAGGCTTGTTCACACGTCACGGC 60
|||||
Db 251 ATGAAGAAGTCTTTCACCGTGGCCATCTTGCTGGCAGGCTTGTTCACACGTCACGGC 60
|||||
Qy 61 AGCCTGCTCAACCTGAAGCCATGTTGGAGGCGTCCACAGAGGAGGAGGCCATCTGTGCC 120
|-Db 311 AGCCTGCTGAACCTGAAGTCCATGTTGGAGGCCATCACACAGAACTCCATCTGTGCC 370
Qy 121 TTGCTGGGCTACGCTGCTACTGTGGCTGGGGGCGGTCGAGGAGGAGGAGGAGGAGGAG 180
Db 371 TTGCTGGGCTACGCTGCTACTCGGGGCTGGGGGCGGTCGAGGAGGAGGAGGAGGAGG 430
Qy 181 GACTGTGTGCCACGCCACGACTGCTGTACGAGAACTTTTGACCAAGGCTGTAC 240
Db 431 GACTGTGTGCCATGCCACGACTGTTGCTATGAGAAGCTTTGAGCAGGCTTGC 490
Qy 241 CCTATGTGACCACTATGATACACCATCGAGAACACACTGAGATGCTGCACTGAG 300
Db 491 CCTATGTGACCACTATGATACACCATCGAGAACACACTGAGATGCTGCACTGAG 550
Qy 301 CTCAACACACAGAGTGTGACAAAGACATGCTGTGACAAACATGTTCTGTGTC 360
Db 551 CTCAATGACAGGAGTGTGACAAAGACATGCTGTGACAAACATGTTCTGTGTC 610
Qy 361 CTCATGAACACAGCTGACGAGAGGAGTACCGTGTCTCAATGTCTACTGCGAGGGC 420
Db 611 CTCGAAGATCACCCATACAGAAACATGCTGTGACAAACATGTTCTACTGCGAGGGC 670
Qy 421 CCCACGCCCAACTGACGATCTATGACCGCCCTGAGGAGGCTACCTGCACTGACCAA 480
Db 671 CCCACGCCCAACTGACGATCTATGACCGCCCTGAGGAGGCTACCTGCACTGACCAA 730
Qy 481 TCCCCAGCGCCCGCCCTCCCTCCCTAG 507
Db 731 CTCCCTGGCAGCCCTCTCTCAACCTAG 757
```

```
RESULT 9
US-60-229-525-724
; Sequence 724, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
```

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; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-724

Query Match 60.2%; Score 305; DB 66; Length 748;
Best Local Similarity 83.2%; Pred. No. 2.1e-65;
Matches 347; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 91 GCCGTACACAGGAGGAGCGGCATCTGCTCTGCTGGGCTACGGTTCCTACTGTGGGCTG 150
Db 171 GCCGTACACAGGAGGAGCGGCATCTGCTCTGCTGGGCTACGGTTCCTACTGTGGGCTG 230
Qy 151 GGGGGCGGTGGCCAGCCCAAGGATGAGGTGACTGTGCTGCCACGCCACGACTGCTGC 210
Db 231 GGGGGCGGTGGCCAGCCCAAGGATGAGGTGACTGTGCTGCCACGCCACGACTGCTGC 290
Qy 211 TACCAGAACTCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCAATC 270
Db 291 GTCAGGGCGCAATGAGGACAGCTGTGCTACCCCTATGTGGACCACTATGATCACCAATC 350
Qy 271 GAGAACAACTGAGATAGTCTGACGTGACCTCAACAAGACAGAGTGTGACAAAGCAGACA 330
Db 351 GAGAACAACTGAGATAGTCTGACGTGACCTCAACAAGACAGAGTGTGACAAAGCAGACA 410
Qy 331 TGCATGTGTGACAAAGACATGTTCTGTGCTCATGAACACAGACAGTACCGAGAGGATAC 390
Db 411 AGGAGTGGCTGGCTTAACATGTTCTGTGCTCATGAACACAGACGTACCGAGAGGATAC 470
Qy 391 CGTGGCTTCTCAATGCTACTGCCAGGGCGCCACGCCCACTGACAGCATCTATGAACGG 450
Db 471 CGTGGCTTCTCAATGCTACTGCCAGGGCGCCACGCCCACTGACAGCATCTATGAACGG 530
Qy 451 CCCCTGAGAGGTGACCTGCTGACGTACCAATCCCCAGCGCCCGCCCTCCCTAG 507
Db 531 CCCCTGAGAGGTGACCTGCTGACGTACCAATCCCCAGCGCCCGCCCTCCCTAG 587

RESULT 10
US-60-229-525-571
; Sequence 571, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-571

Query Match 49.8%; Score 252.4; DB 66; Length 748;
Best Local Similarity 77.9%; Pred. No. 2.6e-52;
Matches 304; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 40 GTTCTGTCACAGCTCACGGAGCTGCTCAACCTGAAGGCACTGGTGAGGGCGTCACA 99
Db 220 GTTCTGTCACAGCTCACGGAGCTGCTCAACCTGAAGGCACTGGTGAGGGCGTCACA 279
Qy 100 GGGAGAGCGGCATCTCTCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159
|||||
```



```
Query Match          41.8%; Score 212; DB 60; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACATGGTTC 355
      |||||||
Db 503 GTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACATGGTTC 444
      |||||||
QY 356 TGTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 415
      |||||||
Db 443 TGTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 384
      |||||||
QY 416 AGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTGCAGTC 475
      |||||||
Db 383 AGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTGCAGTC 324
      |||||||
QY 476 ACCAATCCCCAGCGCCCGCGCCCTCCCTAG 507
      |||||||
Db 323 ACCAATCCCCAGCGCCCGCGCCCTCCCTAG 292
      |||||||

RESULT 14
US-60-207-316-43
; Sequence 43, Application US/60207316
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00605
; CURRENT APPLICATION NUMBER: US/60/207,316
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 4179
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-207-316-43
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Query Match          41.8%; Score 212; DB 64; Length 4179;
Best Local Similarity 100.0%; Pred. No. 4.3e-42;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACATGGTTC 355
      |||||||
Db 1002 GTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACATGGTTC 1061
      |||||||
QY 356 TGTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 415
      |||||||
Db 1062 TGTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 1121
      |||||||
QY 416 AGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTGCAGTC 475
      |||||||
Db 1122 AGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTGCAGTC 1181
      |||||||
QY 476 ACCAATCCCCAGCGCCCGCGCCCTCCCTAG 507
      |||||||
Db 1182 ACCAATCCCCAGCGCCCGCGCCCTCCCTAG 1213
      |||||||
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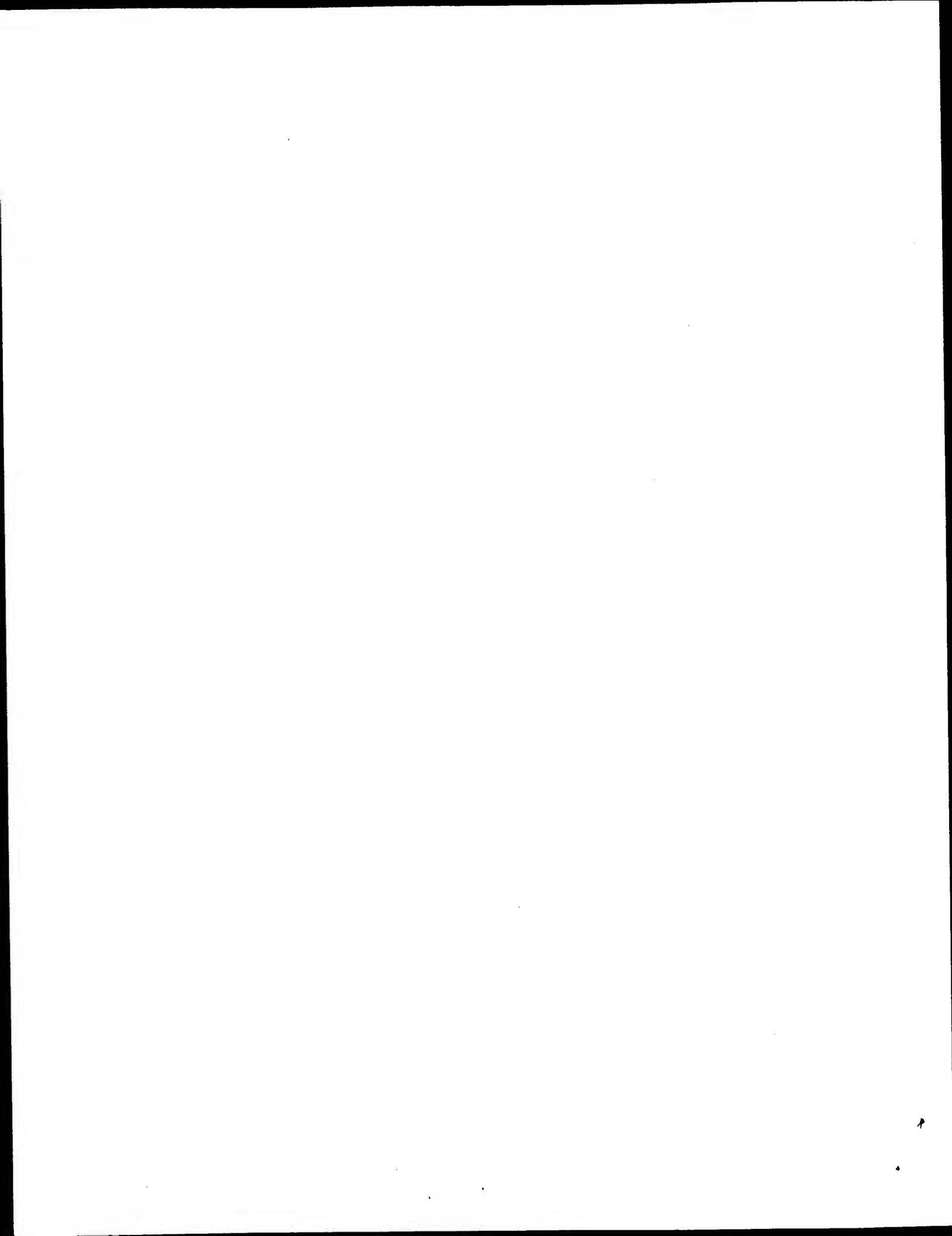
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RESULT 15
US-09-609-137-56
; Sequence 56, Application US/09609137
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-158
; CURRENT APPLICATION NUMBER: US/09/609,137
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 56
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-609-137-56

Query Match          39.3%; Score 199.4; DB 23; Length 1644;
Best Local Similarity 94.9%; Pred. No. 4.8e-39;
Matches 206; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 291 CTGCAGTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACAT 350
      |||||||
Db 45 CTGAGGTGACCTCAACAGACAGAGTGTGACAGACAGATGTCATGTCGACAGAACAT 104
      |||||||
QY 351 GGTTCCTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTA 410
      |||||||
Db 105 GGTTCCTGCTCATGAACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTA 164
      |||||||
QY 411 CTGCCAGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTG 470
      |||||||
Db 165 CTGCCAGGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCGCTGAGGAGGTCACTG 224
      |||||||
QY 471 CAGTCACCAATCCCCAGCGCCCGCGCCCTCCCTAG 507
      |||||||
Db 225 CAATCACAATCCACACCCCGCCCTCCCGCCAG 261
      |||||||

Search completed: February 8, 2003, 06:38:30
Job time : 3119 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:36:59 : Search time 182 Seconds
(without alignments)
3602.321 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

Sequence: 1 atgaagaagtcttcacgt.....cgccccccgccccctccctag 507

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2558245 seqs, 646570469 residues

Total number of hits satisfying chosen parameters: 5116490

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	100.0	2270	6	US-10-275-998-7
2	507	100.0	2297	1	PCN-US02-21338-79
3	507	100.0	2297	6	US-10-188-832-79
4	99	19.5	1327	6	US-10-276-781-616
5	99	19.5	1938	5	US-09-949-002-110
6	99	19.5	1938	5	US-09-949-002-228
7	99	19.5	2747	1	PCN-US02-29560-195
8	99	19.5	2747	6	US-10-245-882-195
9	95.6	18.9	496	6	US-10-131-813A-533
10	95.6	18.9	496	6	US-10-131-819A-533
11	95.6	18.9	496	6	US-10-131-823A-533
12	95.6	18.9	496	6	US-10-131-824A-533
13	95.6	18.9	496	6	US-10-131-826A-533
14	95.6	18.9	496	6	US-10-131-829A-533
15	95.6	18.9	496	6	US-10-125-926A-533
16	95.6	18.9	496	6	US-10-127-829A-533
17	95.6	18.9	496	6	US-10-127-831A-533
18	95.6	18.9	496	6	US-10-127-835A-533
19	95.6	18.9	496	6	US-10-127-837A-533
20	95.6	18.9	496	6	US-10-127-842A-533
21	95.6	18.9	496	6	US-10-127-850A-533
22	95.6	18.9	496	6	US-10-127-901A-533
23	95.6	18.9	496	6	US-10-128-689A-533
24	95.6	18.9	496	6	US-10-131-830A-533
25	95.6	18.9	496	6	US-10-131-833A-533
26	95.6	18.9	496	6	US-10-131-837A-533

27	95.6	18.9	496	6	US-10-125-930A-533	Sequence 533, App
28	95.6	18.9	496	6	US-10-127-825A-533	Sequence 533, App
29	95.6	18.9	496	6	US-10-127-838B-533	Sequence 533, App
30	95.6	18.9	496	6	US-10-127-843A-533	Sequence 533, App
31	95.6	18.9	496	6	US-10-127-849A-533	Sequence 533, App
32	95.6	18.9	496	6	US-10-128-684A-533	Sequence 533, App
33	95.6	18.9	496	6	US-10-128-685A-533	Sequence 533, App
34	95.6	18.9	496	6	US-10-128-686A-533	Sequence 533, App
35	95.6	18.9	496	6	US-10-128-690A-533	Sequence 533, App
36	95.6	18.9	496	6	US-10-128-693A-533	Sequence 533, App
37	95.6	18.9	496	6	US-10-131-821A-533	Sequence 533, App
38	95.6	18.9	496	6	US-10-131-836A-533	Sequence 533, App
39	95.6	18.9	496	6	US-10-137-872A-533	Sequence 533, App
40	95.6	18.9	496	6	US-10-137-873A-533	Sequence 533, App
41	95.6	18.9	496	6	US-10-125-921A-533	Sequence 533, App
42	95.6	18.9	496	6	US-10-125-928A-533	Sequence 533, App
43	95.6	18.9	496	6	US-10-127-821A-533	Sequence 533, App
44	95.6	18.9	496	6	US-10-127-822A-533	Sequence 533, App
45	95.6	18.9	496	6	US-10-127-824A-533	Sequence 533, App

ALIGNMENTS

RESULT 1
US-10-275-998-7

: Sequence 7, Application US/10275998

: GENERAL INFORMATION:

: APPLICANT: INCYTE GENOMICS, INC.

: APPLICANT: DAS, Debopriya

: APPLICANT: REDDY, Roopa

: APPLICANT: YAO, Monique G.

: APPLICANT: NGUYEN, Dannel B.

: APPLICANT: LU, Yan

: APPLICANT: TRIBOULEY, Catherine M.

: APPLICANT: YUE, Henry

: APPLICANT: KHAN, Farrah A.

: APPLICANT: GANDHI, Ameena R.

: APPLICANT: AU-YOUNG, Janice

: APPLICANT: LAL, Preeti

: APPLICANT: KEARNEY, Liam

: APPLICANT: ELLIOTT, Vicki S.

: APPLICANT: DING, Li

: APPLICANT: THORNTON, Michael

: TITLE OF INVENTION: LIPID METABOLISM ENZYMES

: FILE REFERENCE: PI-0095 USN

: CURRENT APPLICATION NUMBER: US/10/275,998

: PRIOR FILING DATE: 2002-11-08

: PRIOR APPLICATION NUMBER: US 01/15210

: PRIOR FILING DATE: 2001-05-11

: PRIOR APPLICATION NUMBER: US 60/203,511

: PRIOR FILING DATE: 2000-05-11

: PRIOR APPLICATION NUMBER: US 60/207,903

: PRIOR FILING DATE: 2000-05-25

: PRIOR APPLICATION NUMBER: US 60/210,150

: PRIOR FILING DATE: 2000-06-07

: PRIOR APPLICATION NUMBER: US 60/213,392

: PRIOR FILING DATE: 2000-06-23

: NUMBER OF SEQ ID NOS: 10

: SOFTWARE: PERL Program

: SEQ ID NO 7

: LENGTH: 2270

: TYPE: DNA

: ORGANISM: Homo sapiens

: FEATURE:

: NAME/KEY: misc.feature

: OTHER INFORMATION: Incyte ID No: 7473224CB1

US-10-275-998-7

Query Match 100.0%; Score 507; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
|||||
Db 222 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 281
|||||
QY 61 AGCTGTCTCAACCTGAAGCCCATGTGGAGGCCGTGCACAGGAGAGAGGCCCATCTGTGCC 120
|||||
Db 282 AGCTGTCTCAACCTGAAGCCCATGTGGAGGCCGTGCACAGGAGAGAGGCCCATCTGTGCC 341
|||||
QY 121 TTGCTGGGCTACCGTTGCTTACTGTGGGCTGGGGCCGCTGGCCAGCCCAAGGATCAGGTG 180
|||||
Db 342 TTGCTGGGCTACCGTTGCTTACTGTGGGCTGGGGCCGCTGGCCAGCCCAAGGATCAGGTG 401
|||||
QY 181 GACTGTGTGGCCACGCCACGACTGCTGTACAGGAACTTTTGAACCAAGGCTGTGCAC 240
|||||
Db 402 GACTGTGTGGCCACGCCACGACTGCTGTACAGGAACTTTTGAACCAAGGCTGTGCAC 461
|||||
QY 241 CCTATGTGGACCACTATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 300
|||||
Db 462 CCTATGTGGACCACTATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 521
|||||
QY 301 CTCACCAAGACAGAGTGTGACAAAGCAGACATGATGTGTGACAAAGCAATGTTCTGTGC 360
|||||
Db 522 CTCACCAAGACAGAGTGTGACAAAGCAGACATGATGTGTGACAAAGCAATGTTCTGTGC 581
|||||
QY 361 CTCATGAACACAGCTTACCGAGAGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGGC 420
|||||
Db 582 CTCATGAACACAGCTTACCGAGAGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGGC 641
|||||
QY 421 CCCACGCCCAACTGACGATCTATGAACGCCGCCCTGAGGAGGTCACTGAGTCAACCA 480
|||||
Db 642 CCCACGCCCAACTGACGATCTATGAACGCCGCCCTGAGGAGGTCACTGAGTCAACCA 701
|||||
QY 481 TCCCCAGCGCCCGCCGCCCTCCCTAG 507
|||||
Db 702 TCCCCAGCGCCCGCCGCCCTCCCTAG 728
|||||

RESULT 2

PCT-US02-21338-79
; Sequence 79, Application PC/TUS0221338
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330PC
; CURRENT APPLICATION NUMBER: PCT/US02/21338
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21338-79

Query Match 100.0%; Score 507; DB 1; Length 2297;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
|||||

Db 249 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 308
|||||
QY 61 AGCTGTCTCAACCTGAAGCCCATGTGGAGGCCGTGCACAGGAGAGAGGCCCATCTGTGCC 120
|||||
Db 309 AGCTGTCTCAACCTGAAGCCCATGTGGAGGCCGTGCACAGGAGAGAGGCCCATCTGTGCC 368
|||||
QY 121 TTGCTGGGCTACCGTTGCTTACTGTGGGCTGGGGCCGCTGGCCAGCCCAAGGATCAGGTG 180
|||||
Db 369 TTGCTGGGCTACCGTTGCTTACTGTGGGCTGGGGCCGCTGGCCAGCCCAAGGATCAGGTG 428
|||||
QY 181 GACTGTGTGGCCACGCCACGACTGCTGTACAGGAACTTTTGAACCAAGGCTGTGCAC 240
|||||
Db 429 GACTGTGTGGCCACGCCACGACTGCTGTACAGGAACTTTTGAACCAAGGCTGTGCAC 488
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QY 241 CCTATGTGGACCACTATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 300
|||||
Db 489 CCTATGTGGACCACTATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 548
|||||
QY 301 CTCACCAAGACAGAGTGTGACAAAGCAGACATGATGTGTGACAAAGCAATGTTCTGTGC 360
|||||
Db 549 CTCACCAAGACAGAGTGTGACAAAGCAGACATGATGTGTGACAAAGCAATGTTCTGTGC 608
|||||
QY 361 CTCATGAACACAGCTTACCGAGAGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGGC 420
|||||
Db 609 CTCATGAACACAGCTTACCGAGAGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGGC 668
|||||
QY 421 CCCACGCCCAACTGACGATCTATGAACGCCGCCCTGAGGAGGTCACTGAGTCAACCA 480
|||||
Db 669 CCCACGCCCAACTGACGATCTATGAACGCCGCCCTGAGGAGGTCACTGAGTCAACCA 728
|||||
QY 481 TCCCCAGCGCCCGCCGCCCTCCCTAG 507
|||||
Db 729 TCCCCAGCGCCCGCCGCCCTCCCTAG 755
|||||

RESULT 3

US-10-188-832-79
; Sequence 79, Application US/10188832
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-832-79

Query Match 100.0%; Score 507; DB 6; Length 2297;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
|||||

Db 249 ATGAAGAAGTTCTTACCGCTGGCCATCTTCTGGCAGCGTTCTGTCCACAGCTCACGGC 308
QY 61 AGCTGCTCAACCTGAAGCCCATGTTGGAGCGGTGCACAGGAGGAGGCCCATCTCTGTCC 120
Db 309 AGCTGCTCAACCTGAAGCCCATGTTGGAGCGGTGCACAGGAGGAGGCCCATCTCTGTCC 368
QY 121 TTGCTGGGTAGCGTTGCTACTGTTGGCTGGGGGGCGGTGGCCAGCCCAAGGATGAGTG 180
Db 369 TTGCTGGGTAGCGTTGCTACTGTTGGCTGGGGGGCGGTGGCCAGCCCAAGGATGAGTG 428
QY 181 GACTGTGCTGCGCAGCCCGCACAGCTGCTGTACACAGGAACTCTTTGACCAAGGCTGTAC 240
Db 429 GACTGTGCTGCGCAGCCCGCACAGCTGCTGTACACAGGAACTCTTTGACCAAGGCTGTAC 488
QY 241 CCTATGTGACCACTATGATCACACCATCGAGACACACTGAGATAGTGTGAGTGCAC 300
Db 489 CCTATGTGACCACTATGATCACACCATCGAGAACAACTGAGATAGTGTGAGTGCAC 548
QY 301 CTCACAGACAGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 360
Db 549 CTCACAGACAGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 608
QY 361 CTCATGAACCACTGACGAGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 420
Db 609 CTCATGAACCACTGACGAGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 668
QY 421 CCCAGCCCAACTGACGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 480
Db 669 CCCAGCCCAACTGACGAGTGTGACAGCAGACATGCTGTGTGACAAAGACATGTTTCTGTGC 728
QY 481 TCCCGAGCGCCCGCCCGCCCTCCCTAG 507
Db 729 TCCCGAGCGCCCGCCCGCCCTCCCTAG 755

RESULT 4
US-10-276-781-616
; Sequence 616, Application US/10276781
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 616
; LENGTH: 1927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-616

Query Match 19.5%; Score 99; DB 6; Length 1927;
Best Local Similarity 57.2%; Pred. No. 2.7e-16;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCCATGGTGGAGGCCGCTCACA 99
Db 57 GGTGTGATTCCCAATCCAGGGCGGGATCTTGAACCTGAACCAAGATGGTCAAGCAAGTACT 116
QY 100 GGGAGGAGCGCCATCTCTGCTTCTGGGCTACGGTGTGCTACTGTGGCTGGGGGCGGT 159
Db 117 GGGAAATGCCCATCTCTCTACTGTGGCCCTACGGCTGTCTACTGTGGGACTAGGTGGCAGA 176
QY 160 GGGAGCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
Db 177 GGGCAACCCCAAGATGCCAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 236
QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCATACACCATCGAACAAC 279

Db 237 CTGAAGACCCAGGGTGGGCATCTACAGGACTATTACAGATACAACCTT-----TTCC 290
QY 280 ACTGAGATAGTCTGCACTGACCTCAACAAAGACAGAGTGTGACAGCAGACATGCTATGTGT 339
Db 291 CAGGGAAACATCCACTGCTCTGACAGGGAAGTGTGTGTGAGCAGCAGCTGTGTGCTCTGT 350
QY 340 GACAAGAACATGTTCTGTGCTCATGAACACAGAGCTACCCGAGAGGAGTACCG 392
Db 351 GACAAGAGGTGGCCTTCTGCTGAAGCGCAACCTGGACACCTACCCAGAAGCG 403

RESULT 5
US-09-949-002-110
; Sequence 110, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-110

Query Match 19.5%; Score 99; DB 5; Length 1938;
Best Local Similarity 57.2%; Pred. No. 2.7e-16;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCCATGGTGGAGGCCGCTCACA 99
Db 76 GGTGTGATTCCCAATCCAGGGCGGGATCTTGAACCTGAACCAAGATGGTCAAGCAAGTACT 135
QY 100 GGGAGGAGCGCCATCTCTGCTTCTGGGCTACGGTGTGCTACTGTGGCTGGGGGCGGT 159
Db 136 GGGAAATGCCCATCTCTCTACTGTGGCCCTACGGCTGTGCTACTGCGGACTAGGTGGCAGA 195
QY 160 GGGAGGAGCGCCATCTCTGCTTCTGGGCTACGGTGTGCTGCCAGCCCAAGCTGCTGCTAC 219
Db 196 GGGCAACCCCAAGATGCCAGGAGTGGTGTGCTGCCAGACCATGCTGCTATGACCAAC 255
QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCATACACCATCGAACAAC 279
Db 256 CTGAAGACCCAGGGTGGCAGCTCTCAAGGACTATTACAGATACAACCTT-----TTCC 309
QY 280 ACTGAGATAGTCTGCACTGACCTCAACAAAGACAGAGTGTGACAAGCAGACATGCTATGTGT 339
Db 310 CAGGGAAACATCCACTGCTCTGACAAGGAAGTGTGTGTGAGCAGCAGCTGTGTGCTCTGT 369
QY 340 GACAAGAACATGTTCTGTGCTCATGACACAGAGCTACCCGAGAGGAGTACCG 392
Db 370 GACAAGAGGTGGCCTTCTGCTGAAGCGCAACCTGGACACCTACCCAGAAGCG 422

RESULT 6
US-09-949-002-228
; Sequence 228, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401

[illegible]

```

RESULT 9
US-10-131-813A-533
; Sequence 533, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550

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; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 533
;
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:

```

```

; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-813A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps

Qy 40 GTTCTGTCCACAGCTTCACGGCAGCGCTGCTCAACCTCAAGGCCATGGTGGAGCGCGGTCA 99
Db 68 GGTGTGATTCCCAATCCAGGGGGGATCCTCAACCTGACACAGTGGTCAAGCAAGTGACT 127
Qy 100 GGGAGAGCGCCATCCTGCTCTTCGTGGGTGACGGTGTGCTACTGTGGCTGGGGGGCCGT 159
Db 128 GGGAAATGGCCCATCCTCTCTACTGTGCCCTACGGGCTGTCACTGGGACTAGGTGGCAGA 187
Qy 160 GGCCAGCCCAAGATGAGGTGGACTGTGTGTGGCCACGGCCACGACTGCTGCTACCAGGA 219
Db 188 GGCCACCCCAAGATGCCACGGACTGGTCTGCCAGACCCATGACTGCTGCTATGACCAC 247
Qy 220 CTTCTTTGACCAAGCTGTCAACCCCTATGTGGACCACTATGATCAACCAT 269
Db 248 CTGAGACCCCAAGGGTGGCGCATCTTACAAGGACACACAAAGACAGCAT 297

```

RESULT 10
US-10-131-819A-533
; Sequence 533, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

```

, TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
,
, TITLE OF INVENTION: ACIDS ENCODING THE SAME
,
, FILE REFERENCE: P3330RIC134
,
, CURRENT APPLICATION NUMBER: US/10/131,819A
,
, PRIOR FILING DATE: 2002-04-24
,
, PRIOR APPLICATION NUMBER: 60/049911
,
, PRIOR FILING DATE: 1997-06-18
,
, PRIOR APPLICATION NUMBER: 60/056974
,
, PRIOR FILING DATE: 1997-08-26
,
, PRIOR APPLICATION NUMBER: 60/059113
,
, PRIOR FILING DATE: 1997-09-17
,
, PRIOR APPLICATION NUMBER: 60/059115
,
, PRIOR FILING DATE: 1997-09-17
,
, PRIOR APPLICATION NUMBER: 60/059117
,
, PRIOR FILING DATE: 1997-09-17
,
, PRIOR APPLICATION NUMBER: 60/059122
,
, PRIOR FILING DATE: 1997-09-17
,
, PRIOR APPLICATION NUMBER: 60/059184
,
, PRIOR FILING DATE: 1997-09-17
,
, PRIOR APPLICATION NUMBER: 60/059263
,
, PRIOR FILING DATE: 1997-09-18
,
, PRIOR APPLICATION NUMBER: 60/059352
,
, PRIOR FILING DATE: 1997-09-19
,
, PRIOR APPLICATION NUMBER: 60/059588
,
, PRIOR FILING DATE: 1997-09-19
,
, Remaining Prior Application data removed - See File Wrapper or PALM.

```

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: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
:
: US-10-131-819A-533
:
: Query Match 18.9%; Score 95.6; DB 6; Length 496;
: Best Local Similarity 63.5%; Pred. No. 1.4e-15;
: Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
:
: QY 40 GTTCTGTCACAGCTCAGCGCAGCCTGCTCAACCTGAAGGCCATGTTGGAGCGCGTCACA 99
:
: DDB 68 GGTGTGATTCCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGTTCAAGCAAGTGACT 127
:
: QY 100 GGGAGGAGCGGCATCCTGTGCTCTTGTGGGCTACGGTTGTACTGTGGGTGGGGGCCGT 159
:
: DDB 128 GGGAAATGCCATCCTCTCTACTGSCCCTACGGGTGTCTACTCGGACTAGGTGGCAGA 187
:
: QY 160 GGCACGCCCAAGATGAGGTGGACTGTGTGTCGCCACGCCACACACTGCTGTACCAAGAA 219
:
: DDB 188 GGCACACCCAAAGATGCCACGGACTGTTGTGCGCAGACCCATGACTGCTGTATGACCAC 247
:
: QY 220 CTCCTTTGACCAAGCTGTCACCCCTATGTGGACCACCTATGATCACACCAT 269
:
: DDB 248 CTGAAGACCCAGGGTGGCGCATCTACAAGGACACACAAAGACGACAT 297
:
:
: RESULT 11
: US-10-131-823A-533
: ; Sequence 533, Application US/10131823A
: ; GENERAL INFORMATION:
: ; APPLICANT: Baker, Kevin P.
: ; APPLICANT: Beresini, Maureen
: ; APPLICANT: DeForge, Laura
: ; APPLICANT: Desnoyers, Luc
: ; APPLICANT: Filvaroff, Ellen
: ; APPLICANT: Gao, Wei-Qiang
: ; APPLICANT: Gerritsen, Mary E.
: ; APPLICANT: Goddard, Audrey
: ; APPLICANT: Godowski, Paul J.
: ; APPLICANT: Gurney, Austin L.
: ; APPLICANT: Sherwood, Steven
: ; APPLICANT: Smith, Victoria
: ; APPLICANT: Stewart, Timothy A.
: ; APPLICANT: Tumas, Daniel
: ; APPLICANT: Watanabe, Colin K
: ; APPLICANT: Wood, William
: ; APPLICANT: Zhang, Zemin
: ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: ; FILE OF INVENTION: ACIDS ENCODING THE SAME
: ; FILE REFERENCE: P3330R1C143
: ; CURRENT APPLICATION NUMBER: US/10/131,823A
: ; CURRENT FILING DATE: 2002-04-24
: ; PRIOR APPLICATION NUMBER: 60/049911
: ; PRIOR FILING DATE: 1997-06-18
: ; PRIOR APPLICATION NUMBER: 60/056974
: ; PRIOR FILING DATE: 1997-08-26
: ; PRIOR APPLICATION NUMBER: 60/059113
: ; PRIOR FILING DATE: 1997-09-17
: ; PRIOR APPLICATION NUMBER: 60/059115
: ; PRIOR FILING DATE: 1997-09-17
: ; PRIOR APPLICATION NUMBER: 60/059117
: ; PRIOR FILING DATE: 1997-09-17
: ; PRIOR APPLICATION NUMBER: 60/059122
: ; PRIOR FILING DATE: 1997-09-17
: ; PRIOR APPLICATION NUMBER: 60/059184
: ; PRIOR FILING DATE: 1997-09-17
: ; PRIOR APPLICATION NUMBER: 60/059263

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-824A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCCACAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGGTGAGGCCGTCACA 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 GGTGTGATTCCATCCAGGGGGGATCTTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127

QY 100 GCGAGAGGCCCATCTCTCTTCTGCGGCTACGGTTGCTACTGTGGGCGGCGGT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 GGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCTGCGGACTAGGTGGCAGA 187

QY 160 GCGCAGCCCAAGGATGAGGTGAGTGGTCTGCCAGGCCACGACTGTGTATGATCACACCAT 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 GGCACACCCAAAGATGCCAGGACTGTGCTGCCAGACCCATGATGCTGTATGACCAAC 247

QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 CTGAAGACCCAGGGGTGGCGCATCTACAAGGACAAACAACAAAGCAGCAT 297

RESULT 13
US-10-131-826A-533
; Sequence 533, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-826A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCCACAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGGTGAGGCCGTCACA 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 GGTGTGATTCCATCCAGGGGGGATCTTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127

QY 100 GCGAGAGGCCCATCTCTCTTCTGCGGCTACGGTTGCTACTGTGGGCGGCGGT 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 GGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCTGCGGACTAGGTGGCAGA 187

QY 160 GCGCAGCCCAAGGATGAGGTGAGTGGTCTGCCAGGCCACGACTGTGTATGATCACACCAT 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 GGCACACCCAAAGATGCCAGGACTGTGCTGCCAGACCCATGATGCTGTATGACCAAC 247

QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 CTGAAGACCCAGGGGTGGCGCATCTACAAGGACAAACAACAAAGCAGCAT 297

RESULT 14
US-10-131-829A-533
; Sequence 533, Application US/10131829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:56 : Search time 143 Seconds
(without alignments)
757.449 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence:

1 MKKFTVAILAGSVLSTAHG.....EPPEVTCSHQSPAPP 168

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pap.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pap.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pap.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pap.*
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16: /cgn2_6/ptodata/1/paa/US092_COMB.pap.*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pap.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	957	100.0	168	23	US-09-975-456B-2
2	957	100.0	211	27	US-60-203-511-2
3	957	100.0	211	27	US-60-403-468-4
4	950	99.3	168	25	US-10-104-047-3735
5	895.5	93.6	275	27	US-60-212-356-145
6	892.5	93.3	248	27	US-60-212-356-180

7	892.5	93.3	248	27	US-60-229-525-298	Sequence 298, App
8	892.5	93.3	248	27	US-60-229-525-451	Sequence 451, App
9	747	78.1	168	21	US-09-791-537-148869	Sequence 148869
10	733	76.6	126	27	US-60-229-525-468	Sequence 468, App
11	460	48.1	85	27	US-60-234-446-626	Sequence 626, App
12	353	36.9	145	1	PCT-US01-10542-17	Sequence 17, Appl
13	353	36.9	145	23	US-09-969-384-17	Sequence 17, Appl
14	353	36.9	145	23	US-09-975-456B-7	Sequence 7, Appl
15	352	36.8	145	1	PCT-US01-12529A-6	Sequence 6, Appl
16	352	36.8	145	15	US-09-181-317-1	Sequence 1, Appl
17	352	36.8	145	15	US-09-791-537-140100	Sequence 1, Appl
18	352	36.8	145	22	US-09-835-996A-6	Sequence 6, Appl
19	352	36.8	145	22	US-09-856-486-27	Sequence 27, Appl
20	352	36.8	150	1	PCT-US00-35017A-1342	Sequence 1342, Ap
21	344.5	36.0	144	21	US-09-791-537-148830	Sequence 148830,
22	344.5	36.0	144	22	US-09-856-486-14	Sequence 14, Appl
23	344	35.9	299	27	US-60-212-356-144	Sequence 144, App
24	344	35.9	299	27	US-60-229-525-452	Sequence 452, App
25	340.5	35.6	134	27	US-60-207-316-109	Sequence 109, App
26	319.5	33.4	138	21	US-09-791-537-21221	Sequence 21221, A
27	313.5	32.8	142	21	US-09-791-537-148806	Sequence 148806,
28	312	32.6	118	21	US-09-791-537-131157	Sequence 131157,
29	309.5	32.3	138	21	US-09-791-537-78689	Sequence 78689, A
30	309	32.3	142	21	US-09-791-537-15988	Sequence 15988, A
31	309	32.3	154	23	PCT-US02-23913-325	Sequence 325, App
32	302.5	31.6	144	1	US-08-046-383-10	Sequence 10, Appl
33	302.5	31.6	144	4	US-08-091-941-37	Sequence 37, Appl
34	302.5	31.6	144	4	US-08-463-958-37	Sequence 37, Appl
35	302.5	31.6	144	8	US-08-651-405-37	Sequence 37, Appl
36	302.5	31.6	144	10	US-09-791-537-4717	Sequence 4717, Ap
37	302.5	31.6	144	23	US-09-975-456B-6	Sequence 6, Appl
38	302.5	31.6	144	25	US-10-116-275-269	Sequence 269, App
39	302.5	31.6	144	26	US-10-205-823-325	Sequence 325, App
40	302.5	31.6	164	1	PCT-US00-05988-1010	Sequence 1010, Ap
41	302.5	31.6	164	13	US-08-973-602-29	Sequence 29, Appl
42	302.5	31.6	164	20	US-09-646-777A-246	Sequence 246, App
43	302.5	31.6	164	23	US-09-925-300-1010	Sequence 1010, Ap
44	302.5	31.6	164	23	US-09-791-537-139699	Sequence 139699,
45	298.5	31.2	122	21		

ALIGNMENTS

RESULT 1
US-09-975-456B-2
: Sequence 2, Application US/09975456B
: GENERAL INFORMATION:
: APPLICANT: LAZDUNSKI, MICHEL
: APPLICANT: LAMBEAU, GERARD
: APPLICANT: VALENTIN, EMMANUEL
: TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
: FILE REFERENCE: 1478-R-00
: CURRENT APPLICATION NUMBER: US/09/975,456B
: PRIOR FILING DATE: 2002-08-27
: PRIOR APPLICATION NUMBER: 60/239,491
: PRIOR FILING DATE: 2000-10-11
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn version 2.1
: SEQ ID NO 2
: LENGTH: 168
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-975-456B-2

Query Match 100.0% Score 957; DB 23; Length 168;
Best Local Similarity 100.0%; Pred. No. 4.2e-85;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKFTVAILAGSVLSTAHGSLNLKAMVEATGRSAILSVFGYCGYCGGGRQPKDEV 60
|||||
Db 1 MKKFTVAILAGSVLSTAHGSLNLKAMVEATGRSAILSVFGYCGYCGGGRQPKDEV 60
|||||

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 44 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
 QY 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 DB 104 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 163
 QY 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168
 DB 164 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 211

RESULT 4

US-10-104-047-3735
 ; Sequence 3735, Application US/10104047
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; PRIOR FILING DATE: 2002-03-25
 ; CURRENT FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3735
 ; LENGTH: 168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 99.3%; Score 950; DB 25; Length 168;
 Best Local Similarity 99.4%; Pred. No. 2e-84;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 1 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 QY 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 DB 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 QY 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168
 DB 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168

RESULT 5

US-60-212-356-145
 ; Sequence 145, Application US/60212356
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
 ; NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 ; FILE REFERENCE: CL000677
 ; CURRENT APPLICATION NUMBER: US/60/212,356
 ; CURRENT FILING DATE: 2000-06-19
 ; NUMBER OF SEQ ID NOS: 411
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 145
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 93.6%; Score 895.5; DB 27; Length 275;
 Best Local Similarity 87.7%; Pred. No. 7.8e-79;
 Matches 164; Conservative 1; Mismatches 3; Indels 19; Gaps 3;

QY 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 DB 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 QY 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168
 DB 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168

RESULT 2

US-60-203-511-2
 ; Sequence 2, Application US/60203511
 ; GENERAL INFORMATION:
 ; APPLICANT: Das, Debopriya
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Rao, Monique G.
 ; APPLICANT: Nguyen, Daniel B.
 ; APPLICANT: Lu, Yan
 ; APPLICANT: Tribouley, Catherine M.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Khan, Farrah A.
 ; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
 ; FILE REFERENCE: PI-0095 P
 ; CURRENT APPLICATION NUMBER: US/60/203,511
 ; CURRENT FILING DATE: 2000-05-11
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 100.0%; Score 957; DB 27; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5.4e-85;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 44 MKKFTTVAAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
 QY 61 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 120
 DB 104 DMCCHADCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNVLC 163
 QY 121 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 168
 DB 164 LMNQTYREYRGFLNVYCGPTPNCISYEPPPEEVTCSHQSPPAPP 211

RESULT 3

US-60-403-468-4
 ; Sequence 4, Application US/60403468
 ; GENERAL INFORMATION:
 ; APPLICANT: Silos-Santiago, Immaculada
 ; TITLE OF INVENTION: Methods and compositions for treating
 ; TITLE OF INVENTION: urological disorders using 260, 55089 or 21407
 ; FILE REFERENCE: MP102-148P1(M)
 ; CURRENT APPLICATION NUMBER: US/60/403,468
 ; CURRENT FILING DATE: 2002-08-14
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: homosapiens
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 100.0%; Score 957; DB 27; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5.4e-85;

Qy	1	MKKFTTVA	IAGSVLSTAHGSLNLKAMVEAVTGTSAILSFVGYCCYCGLGGRGPDPDEV	60
Db	44	MKKFTTVA	IAGSVLSTAHGSLNLKAMVEAVTGTSAILSFVGYCCYCGLGGRGPDPDEV	103
Qy	61	DMCCHAHDC	CYQLFDDGGCHPYVDHYDHTIENNTIEVSDLNKTCECKQTCDMCKNNWLC	120
Db	104	DMCCHAHDC	CYQLFDDGGCHPYVDHYDHTIENNTIEVSDLNKTCECKQTCDMCKNNWLC	163
Qy	121	LNNQTYREEYR	GFLNVYCQGTPTNCISYEPPPEEV-----TC-----SHQSAPPA	166
Db	164	LNNQTYREEYR	GFLNVYCQGTPTNCISYEPPPEEVHLLTCTPSLNSGSAASTEPAPPA	223
Qy	167	-----pp	168	
Db	224	RKLKPP	230	

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Query Match      93.3%; Score 892.5; DB 27; Length 248;
Best Local Similarity 94.6%; pred. No. 1.4e-78;
Matches 159; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKKFFTVAIIAGSLVSTAHGSLLLNKAWVENVGTGRSAILSVFGYGCYGLGGRGQPKDEV 60
Db 44 MKKFFTVAIIAGSLVSTAHGSLLLNKAWVENVGTGRSAILSVFGYGCYGLGGRGQPKDEV 103

QY 61 DMCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTIEVCSDLNKTECDKOTCMCDKNVLC 120
Db 104 DMCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTIEVCSDLNKTECDKOTCMCDKNVLC 163

QY 121 LNNQTYREYRGFLNVYCGQTPNCISYEPPEPVCVTSQSPAPP 168
Db 164 LNNQTYREYRGFLNVYCGQTPNCISYEPPEPVCVTSQSPAPP 210

```

Query Match	93.3%	Score 892.5	DB 27	Length 248
Best Local Similarity	94.6%	pred. No. 14e-78		
Matches 159	Conservative 2	Mismatches 6	Indels 1	Gaps
QY	1	MKKFTFTVAILAGSVLSTAHGSLLNKKAMVEAVTGRSAILSFVGYGCVGCLGGRGQPKDEV	60	
Db	44	MKKFTFTVAILAGSVLSTAHGSLLNKKAMVEAVTGRSAILSFVGYGCVGCLGGRGQPKDEV	103	
QY	61	DWCCHAHDCCYQELFDGQGHPPYVDHYDHTTENNTEIVCSDLNKTECDKQTCMCDKNWVLC	120	
Db	104	DWCCHAHDCCYQELFDGQGHPPYVDHYDHTTENNTEIVCSDLNKTECDKQTCMCDKNWVLC	163	
QY	121	LMNNTYREEYRGFLUNVYCOGPTNCSTIYEPDPEVTCSHQSPAPPAPP	168	
Db	164	LMNNTYREEYRGFLUNVYCOGPTNCSTIYEPDPEVTCSHQSPAPPAPP	210	

Query Match	93.3%	Score 892.5	DB 27	Length 248
Best Local Similarity	94.6%	pred. No. 1.4e-78		
Matches 159	Conservative	2	Mismatches 6	Indels 1
Gaps				1

Qy	1	MKKFTT	VAILAGSVLSTAHGSL	LLNKAMVEAVTGRS	SATLSFVGYGCYGLGRRGQPKDEV	60
Db	44	MKKFTT	VAILAGSVLSTAHGSL	LLNKAMVEAVTGRS	SATLSFVGYGCYGLGRRGQPKDEV	103
Qy	61	DWCCHADCCYQELF	DQGCHPYVDHYDHT	IENNTEIVCSDLN	LTKTCQKOTCMCDKNMVL	120
Db	104	DWCCHADCCYQELF	DQGCHPYVDHYDHT	IENNTEIVCSDLN	LTKTCQKOTCMCDKNMVL	163
Qy	121	LMNQTYYREYRGFL	NVYCOGPTPNC	SYEPPEVTCSH	SPAPP	168
Db	164	LMNQTYYREYRGFL	NVYCOGPTPNC	SYEPPEVTCSH	SPAPP	210

Mon Feb 10 11:36:16 2003

Query Match 78.1%; Score 747; DB 21; Length 168;
 Best Local Similarity 75.2%; Pred. No. 1.5e-64;
 Matches 124; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKFFETVATLSTAGSLVSTAGSLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEV 60
 DB 1 MKFFFAIVLAGSVVTAHSSLNLKSMVEATHRNSILSFVGYGCGGLGGRGHPDEV 60
 QY 61 DMCCHADCCYQELFDQGGHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVL 120
 DB 61 DMCCHADCCYQELFDQGGHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCECKSLTLC 120
 QY 121 LMQTTRREYRGFLNVCYCGPNCISYVPEPPPEVTCGSHQSPAPP 165
 DB 121 LKDHPRNRYKGYFNVCYCGPNCISYDYPPEVTCGSHGLPATP 165

RESULT 10
 US-60-229-525-468
 ; Sequence 468, Application US/60229525
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL000772
 ; CURRENT APPLICATION NUMBER: US/60/229,525
 ; CURRENT FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 819
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 468
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; ORGANISM: HUMAN
 US-60-229-525-468

Query Match 76.6%; Score 733; DB-27; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.6e-63;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GSLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEVDMCCHADCCYQELFDQGC 79
 DB 1 GSLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEVDMCCHADCCYQELFDQGC 60
 QY 80 HPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCLMNAQTREYRGFLNVCYQ 139
 DB 61 HPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCLMNAQTREYRGFLNVCYQ 120
 QY 140 GTPNC 145
 DB 121 GTPNC 126

RESULT 11
 US-60-234-446-626
 ; Sequence 626, Application US/60234446
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000832
 ; CURRENT APPLICATION NUMBER: US/60/234,446
 ; CURRENT FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 1797
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 626
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; ORGANISM: HUMAN
 US-60-234-446-626

Query Match 48.1%; Score 460; DB 27; Length 85;

Best Local Similarity 98.8%; Pred. No. 8.8e-37;
 Matches 79; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 21 SLLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEVDMCCHADCCYQELFDQGC 80
 DB 1 SLLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEVDMCCHADCCYQELFDQGC 60
 QY 81 PYVDHYDHTIENNTIIVCS 100
 DB 61 PYVDHYDHTIENNTIIVCSE 80

RESULT 12
 PCT-US01-10542-17
 ; Sequence 17, Application PC/TUS0110542
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Human Gene Sequence Polynucleotides, Polypeptides, and Antibod
 ; FILE REFERENCE: PT055PCT
 ; CURRENT APPLICATION NUMBER: PCT/US01/10542
 ; CURRENT FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: 60/236,384
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/194,118
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 PCT-US01-10542-17

Query Match 36.9%; Score 353; DB 1; Length 145;
 Best Local Similarity 45.5%; Pred. No. 5e-26;
 Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA---HGSLNLKAMVEAVTGRSAILSFVGYGCGGLGGRGQPKDEVDM 62
 DB 3 LALLCGLVVMAGVPIQGILLNLKMKVQVTKMPLSYWPGYCHGCGGLGGRGQPKDATDW 62
 QY 63 CCHADCCYQELFDQGGHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCLM 122
 DB 63 CCQTHDCCYDHLKTCGCSIYKDYRYNFSQ-NIHCS-D-RGSWCEQQLCACDKEVAFCLK 120
 QY 123 N-QTYREYRGFLNVCYCGPNC 145
 DB 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145

RESULT 13
 US-09-969-384-17
 ; Sequence 17, Application US/09969384
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore, et al.
 ; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
 ; FILE REFERENCE: PT055P1
 ; CURRENT APPLICATION NUMBER: US/09/969,384
 ; CURRENT FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: PCT/US01/10542
 ; PRIOR FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: 60/236,384
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/194,118
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-969-384-17

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Query Watch      36.9%  Score 353;  DB 23;  Length 145;
Best Local Similarity 45.5%;  Pred. No. 5e-26;
Matches 66;  Conservative 19;  Mismatches 52;  Indels 8;  Gaps 4;

QY      7  VALAGSVLSTA----HCSLLNLKAMVEATGTSAILSFFVGYCYGGLGRGQPKDEVDW 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3  LALLCGLVVMAGVPTIOGGILNLNKNKVKQVTGMPILSYWYPYCHGGLGRGQPKDATDW 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY     63  CCHAHDCCYQELFQDGHYPYVDHYDHTIENNTLVCSDLNKTCDKQTQCMCKNNVLCLM 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     63  CCQTHDCCYVDHLKTQGSYIKDYRYNFSOG-NIHCSW-EGQQLACADKEVAFCLK 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY     123  N--QTYREERYGFLNVYCGQPTPMC 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     121  RNLDTYQKRLLFYWRPHRCGOTPGC 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Query Match	36.9%	Score	353	DB	23	Length	145
Best Local Similarity	45.5%	Pred	No. 5e-26				
Matches	66	Conservative	19	Mismatches	52	Indels	8
Gaps	4						
QY	7	VALLAGSVLSTA----	HGSLNLNKAMYEAVTGRSAILSFVGYCYGGLGGRQPKDEVDW	62			
Db		: : : : : :	: : : : : :	: : : : : :			
	3	LALLCGLVMVAGVIP	IOGGLNLNKMVKQVTGMPILSYWPGCHGLGGRQPKDATDW	62			
QY	63	CGAHDDCCYQLEFGDCHPYVDYDHT	TIENNTIIVCSDLNKTCDKQTCQMCDDKNVLCLM	122			
Db		: : : : : :	: : : : : :	: : : : : :			
	63	CGQTHDCCYDHLKTQGSISYKDIYRNF	SOG-NIHCSD-KGSWCQQLCACDKEVAFCLK	120			
QY	123	N--QTYREYRGFLNVYCGQPTPNC	145				
Db		: : : : : :	: : : : : :				
	121	RNLDTYQKRLLRYWRPHRCGTGTC	145				

```

; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-12529A-6

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Query Match          36.8%;   Score 352;   DB 1;   Length 145;
Best Local Similarity 45.5%;   Pred. No. 6.2e-26;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

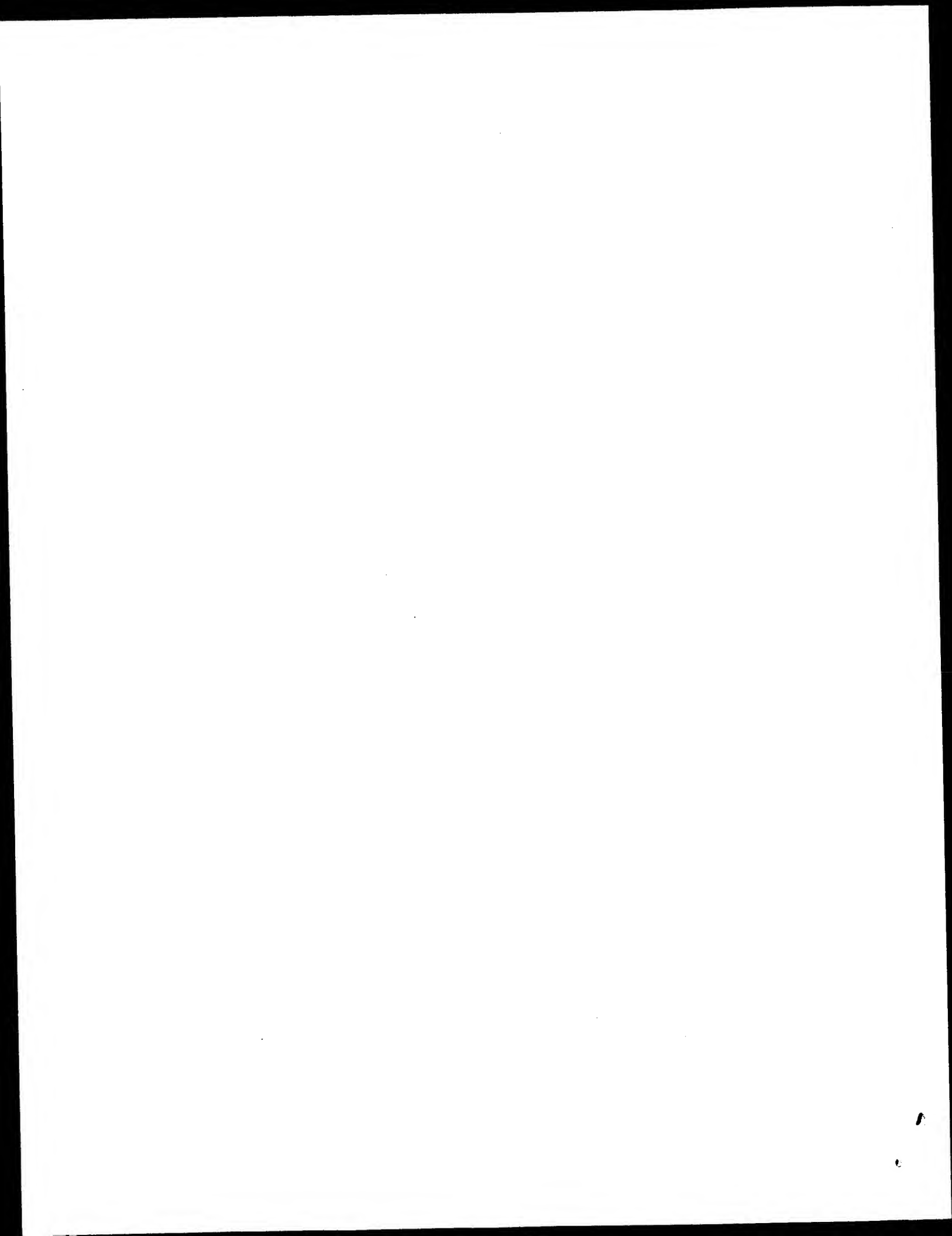
QY      7  VAILAGSVLSTA----HCSLNLNKNMVEATGTSAILSFVGYCYCGLGGRGQPRDEWD 62
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3  LALLCGLVVMAGVIPFGGILNLNKNMKVQTKMNPILSYWYPYCHGGLGGRGQPKDATDW 62
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     63  CCHAHDCCYQOELFGDGHYPYVDHYDHTIENNTETVCSDLNKTBCDKQTCMCDKNVLCGLM 122
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     63  CCOTHDCCYDHLKTQCGGYYKDYRYNFSOG-NIHCSD-KGSWCEQGLACACDKVEAFCLK 120
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY     123  N-QTYREERYGFLNVYCGQFTPMC 145
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     121  RNLDTYQKRLRFYWRPHRCGQTGCG 145
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: February 10, 2003, 10:40:26
Job time : 145 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:36:37 ; Search time 22 Seconds
(without alignments)
619.147 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 405691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957	100.0	211	1	PCT-US02-21338-80
2	957	100.0	211	6	US-10-188-832-80
3	957	100.0	211	6	US-10-275-998-2
4	353	36.9	145	1	PCT-US02-29560-363
5	353	36.9	145	5	US-09-949-002-396
6	353	36.9	145	6	US-10-245-882-363
7	353	36.9	145	5	US-09-949-002-514
8	352	36.8	145	6	US-10-276-781-1625
9	273.5	28.6	116	6	US-10-131-813A-534
10	273.5	28.6	116	6	US-10-131-819A-534
11	273.5	28.6	116	6	US-10-131-823A-534
12	273.5	28.6	116	6	US-10-131-824A-534
13	273.5	28.6	116	6	US-10-131-826A-534
14	273.5	28.6	116	6	US-10-131-829A-534
15	273.5	28.6	116	6	US-10-125-926A-534
16	273.5	28.6	116	6	US-10-127-829A-534
17	273.5	28.6	116	6	US-10-127-831A-534
18	273.5	28.6	116	6	US-10-127-835A-534
19	273.5	28.6	116	6	US-10-127-837A-534
20	273.5	28.6	116	6	US-10-127-842A-534
21	273.5	28.6	116	6	US-10-127-850A-534
22	273.5	28.6	116	6	US-10-127-901A-534
23	273.5	28.6	116	6	US-10-128-689A-534
24	273.5	28.6	116	6	US-10-131-830A-534
25	273.5	28.6	116	6	US-10-131-833A-534
26	273.5	28.6	116	6	US-10-131-837A-534

27	273.5	28.6	116	6	US-10-125-930A-534	Sequence 534, App
28	273.5	28.6	116	6	US-10-127-825A-534	Sequence 534, App
29	273.5	28.6	116	6	US-10-127-838B-534	Sequence 534, App
30	273.5	28.6	116	6	US-10-127-843A-534	Sequence 534, App
31	273.5	28.6	116	6	US-10-127-849A-534	Sequence 534, App
32	273.5	28.6	116	6	US-10-128-684A-534	Sequence 534, App
33	273.5	28.6	116	6	US-10-128-685A-534	Sequence 534, App
34	273.5	28.6	116	6	US-10-128-686A-534	Sequence 534, App
35	273.5	28.6	116	6	US-10-128-690A-534	Sequence 534, App
36	273.5	28.6	116	6	US-10-128-693A-534	Sequence 534, App
37	273.5	28.6	116	6	US-10-131-821A-534	Sequence 534, App
38	273.5	28.6	116	6	US-10-131-836A-534	Sequence 534, App
39	273.5	28.6	116	6	US-10-137-872A-534	Sequence 534, App
40	273.5	28.6	116	6	US-10-137-873A-534	Sequence 534, App
41	273.5	28.6	116	6	US-10-125-921A-534	Sequence 534, App
42	273.5	28.6	116	6	US-10-125-928A-534	Sequence 534, App
43	273.5	28.6	116	6	US-10-127-821A-534	Sequence 534, App
44	273.5	28.6	116	6	US-10-127-822A-534	Sequence 534, App
45	273.5	28.6	116	6	US-10-127-824A-534	Sequence 534, App

ALIGNMENTS

RESULT 1

PCT-US02-21338-80
; Sequence 80, Application PC/TUS0221338
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; FILE REFERENCE: 018501-002330PC
; CURRENT APPLICATION NUMBER: PCT/US02/21338
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-21338-80

Query Match 100.0%; Score 957; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSPVGYGCVGLGGRCQPKDEV	60
DB	44	MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSPVGYGCVGLGGRCQPKDEV	103
QY	61	DWCCHAHCCYQELFDQGCCHPYVDHYDHTTENNTFVCSDLNKTCDKQTCMCDKNVLC	120
DB	104	DWCCHAHCCYQELFDQGCCHPYVDHYDHTTENNTFVCSDLNKTCDKQTCMCDKNVLC	163
QY	121	LMNQTYREYRGFLNVYCOGTPNCISYEPPEVTCSHQSPAPP	168
DB	164	LMNQTYREYRGFLNVYCOGTPNCISYEPPEVTCSHQSPAPP	211

RESULT 2

Mon Feb 10 11:36:17 2003

```
US-10-188-832-80
; Sequence 80, Application US/10188832
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-00233005
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 80
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-80

Query Match      100.0%; Score 957; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
DB 44 MKKFTVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
QY 61 DMCCHADCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCKNNVLC 120
DB 104 DMCCHADCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCKNNVLC 163
QY 121 LMNQTREYRGFLNVYCGQTPNCISYIEPPPEVTCSHOSPAPP 168
DB 164 LMNQTREYRGFLNVYCGQTPNCISYIEPPPEVTCSHOSPAPP 211

US-10-275-998-2
; Sequence 2, Application US/10275998
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YOE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
; PRIOR FILING DATE: 2001-05-11
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US-10-275-998-2
; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No: 7473224CD1
US-10-275-998-2

Query Match      100.0%; Score 957; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
DB 44 MKKFTVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
QY 61 DMCCHADCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCKNNVLC 120
DB 104 DMCCHADCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCKNNVLC 163
QY 121 LMNQTREYRGFLNVYCGQTPNCISYIEPPPEVTCSHOSPAPP 168
DB 164 LMNQTREYRGFLNVYCGQTPNCISYIEPPPEVTCSHOSPAPP 211

PCT-US02-29560-363
; Sequence 363, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 363
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-363

Query Match      36.9%; Score 353; DB 1; Length 145;
Best Local Similarity 45.5%; Pred. No. 8.3e-28;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 62
DB 3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSTWPTGCHGCGYGLGGRGQPKD 62
QY 63 CCHADCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCKNNVLC 122
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PRIOR APPLICATION NUMBER: US 60/355,145

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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-819A-534

Query Match      28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VALLAGSVLSTA---HGSLLNLKNAVEATGSRATLSFVGVCYGLGGRGQPKDEVDW 62
DB 3 LALLGLGVWAGVPIQGGTILNLKMKVQTKMPILSYWPYCHGCHGGLGGRGQPKDATDW 62
QY 63 CCHADCCYQBLFQDQGHVVDHYDHTIENTNTEIVGSDLNKTECKQTCMCDKNMVLCLM 122
DB 63 CCQTHDCCYDHLKTKGGGTYKDN-----NKSSIHCMDLTSQRYC-----LMAVVF 105

QY 123 NOTYRE 128
DB 106 NVIVLE 111

RESULT 10
US-10-131-819A-534
; Sequence 534, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC134
; CURRENT APPLICATION NUMBER: US/10/131,819A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263

```

```

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1625
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-781-1625

Query Match 36.8%; Score 352; DB 6; Length 145;
Best Local Similarity 45.5%; Pred. No. 1e-27;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

ay 7 VAILAGSVLSTA---HGSLINKAMVEAVTGRSATSILSVGVCYGLGGRGQPKDEVDM 62
bb :||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
bb 3 LALCGLGVWAGVPIPOGGILNKVKVKQVTKGMPILSWPYGCHGILGGRGQPKDATDM 62
ay 63 CCHARDCCQGELEFDQGHVPYVDHYDHTIENNTETIVCSLNDKTECHKQTCMDCKNNVLCLM 122
bb :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
bb 63 CCQTHDCCYDHLTKTQGGIYKDYRYNFSQG-NIHGSD-KGSWCQQLCACDKKEVAFCLK 120
ay 123 N-QTYREERYGFLNVCQGPTEPC 145
bb :||| ||| :||| ||| |||
bb 121 RNLDYQKRLRFYWRPHCRGQTGEC 145

RESULT 9
US-10-131-813A-534
; Sequence 534, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1G139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059124

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```

: APPLICANT: Zhang, Zemin
:
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
:
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
:
: FILE REFERENCE: P3330R1C143
:
: CURRENT APPLICATION NUMBER: US/10/131,823A
:
: CURRENT FILING DATE: 2002-04-24
:
: PRIOR APPLICATION NUMBER: 60/049911
:
: PRIOR FILING DATE: 1997-06-18
:
: PRIOR APPLICATION NUMBER: 60/056974
:
: PRIOR FILING DATE: 1997-08-26
:
: PRIOR APPLICATION NUMBER: 60/059113
:
: PRIOR FILING DATE: 1997-09-17
:
: PRIOR APPLICATION NUMBER: 60/059115
:
: PRIOR FILING DATE: 1997-09-17
:
: PRIOR APPLICATION NUMBER: 60/059117
:
: PRIOR FILING DATE: 1997-09-17
:
: PRIOR APPLICATION NUMBER: 60/059122
:
: PRIOR FILING DATE: 1997-09-17
:
: PRIOR APPLICATION NUMBER: 60/059184
:
: PRIOR FILING DATE: 1997-09-17
:
: PRIOR APPLICATION NUMBER: 60/059263
:
: PRIOR FILING DATE: 1997-09-18
:
: PRIOR APPLICATION NUMBER: 60/059352

```

```

1 APPLICANT: Zhang, Zemin
2
3 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
4
5 TITLE OF INVENTION: ACIDS ENCODING THE SAME
6
7 FILE REFERENCE: P3330R1C126
8
9 CURRENT APPLICATION NUMBER: US/10/131,824A
10
11 CURRENT FILING DATE: 2002-04-24
12
13 PRIOR APPLICATION NUMBER: 60/049911
14
15 PRIOR FILING DATE: 1997-06-18
16
17 PRIOR APPLICATION NUMBER: 60/056974
18
19 PRIOR FILING DATE: 1997-08-26
20
21 PRIOR APPLICATION NUMBER: 60/059113
22
23 PRIOR FILING DATE: 1997-09-17
24
25 PRIOR APPLICATION NUMBER: 60/059115
26
27 PRIOR FILING DATE: 1997-09-17
28
29 PRIOR APPLICATION NUMBER: 60/059117
30
31 PRIOR FILING DATE: 1997-09-17
32
33 PRIOR APPLICATION NUMBER: 60/059122
34
35 PRIOR FILING DATE: 1997-09-17
36
37 PRIOR APPLICATION NUMBER: 60/059184
38
39 PRIOR FILING DATE: 1997-09-17
40
41 PRIOR APPLICATION NUMBER: 60/059263
42
43 PRIOR FILING DATE: 1997-09-18
44
45 PRIOR APPLICATION NUMBER: 60/059352
46
47 PRIOR FILING DATE: 1997-09-19
48
49 PRIOR APPLICATION NUMBER: 60/059588
50

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; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-824A-534

Query Match      28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VAILAGSVLSTA-----HGSLLNLKAMWEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLGGLVVMAGVPIQGGILNLNLMKMKVQVTGKMPILSYWPGYCHGCGLGRGQPKDATDW 62

QY 63 CCHAHDCCYQELFDGCHPYVDYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNMVLCLM 122
   ||| ||||| ||| ||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 63 CCQTHDCCYDHLKTGGCGIYKDN-----NKSSIHCMDSQRYC-----LMAVF 105

QY 123 NOTYRE 128
   | | |
Db 106 NVIYLE 111
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```
RESULT 13
US-10-131-826A-534
; Sequence 534, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-534

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Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

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QY 123 NOTYRE 128
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US-10-131-829A-534
; Sequence 534, Application US/10131829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C138
; CURRENT APPLICATION NUMBER: US/10/131,829A
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
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us-09-975-456b-2.rapn

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; ORGANISM: Homo Sapien
US-10-125-926A-534

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Query Match 42.9%; Pred. NO. 5.7e-20;
Best Local Similarity 15; Mismatches 36; Indels 21; Gaps 3;
Matches 54; Conservative

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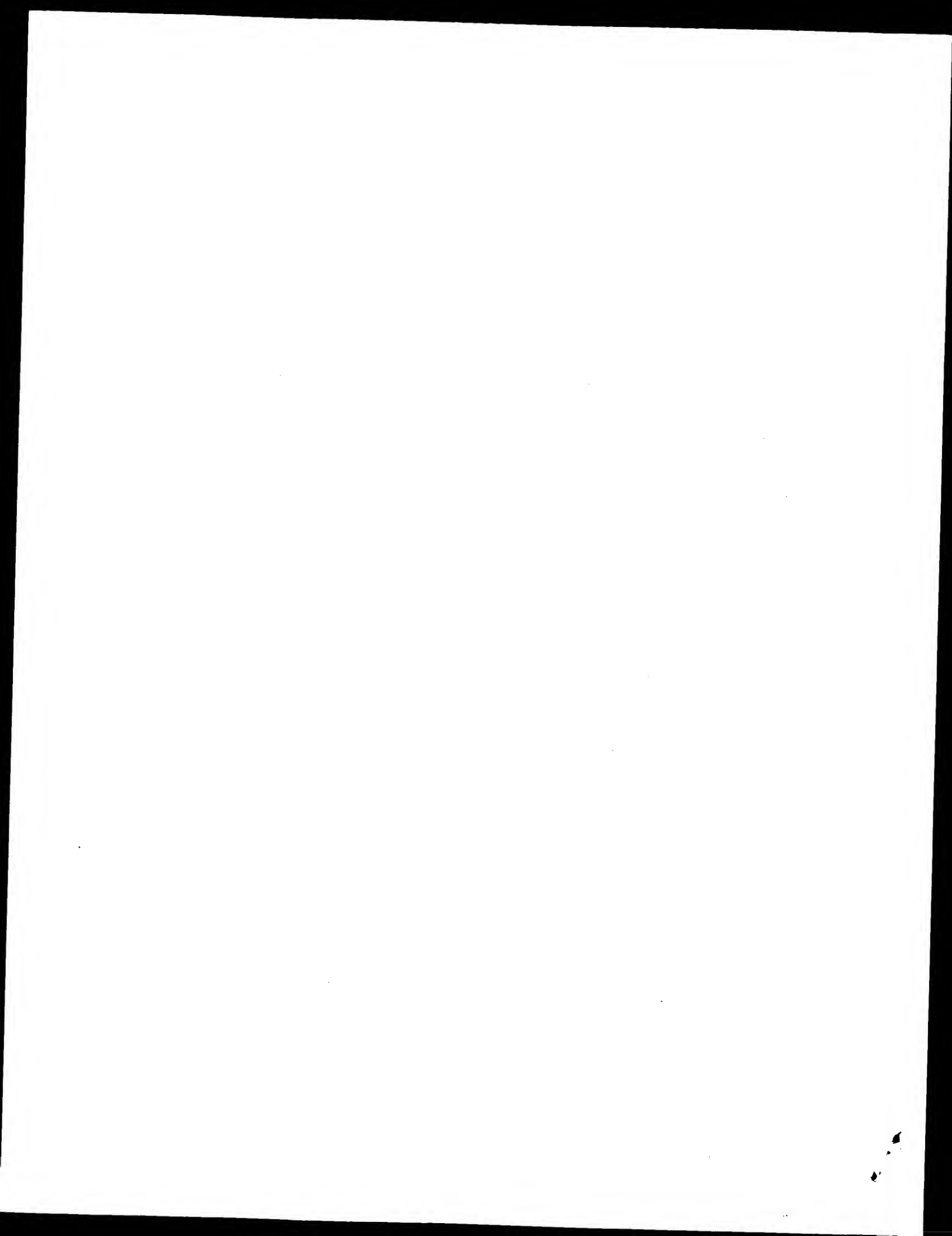
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; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 00:10:29 : Search time 2609 Seconds
(without alignments)
5655.470 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	507	100.0	507	9	AF306566	Homo sapi
2	507	100.0	2270	6	AX304469	Sequence
3	505.4	99.7	2716	9	AK093645	Homo sapi
4	340.6	67.2	906	10	AF166099	Mus muscu
5	212	41.8	135571	9	HS340N1	298257 Human DNA s
6	148	29.2	98743	9	AL158172	Human DNA
7	135.8	26.8	186589	2	AL844178	AL844178 Mus muscu
8	129.4	25.5	157317	2	AC118094	AC118094 Rattus no
9	129.4	25.5	176574	2	AC106106	AC106106 Rattus no
10	99	19.5	878	9	AF112982	Homo sapi
11	99	19.5	1938	9	AF118625	Homo sapi
12	99	19.5	2747	9	BC025706	BC025706 Homo sapi
13	95.6	18.9	496	6	AX464400	Sequence
14	93.2	18.4	1445	10	MMU18119	MMU18119 Mus muscu
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16	91.2	18.0	157317	2	AC118094	AC118094 Rattus no
17	88	17.4	4325	6	AR081988	AR081988 Sequence
18	88	17.4	4325	6	AR198384	AR198384 Sequence
19	88	17.4	4372	10	RRU07798	RRU07798 Rattus norv
20	87.4	17.2	1913	10	AF162713	AF162713 Mus muscu
21	84.2	16.6	414	10	MMU66873	MMU66873 Mus muscu
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39	71.2	14.0	487	6	BD013155	BD013155 A gene en
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42	69.4	13.7	98743	9	AL158172	AL158172 Human DNA
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION AF306566 Homo sapiens group IIF secreted phospholipase A2 mRNA, complete cds.
ACCESSION AF306566
VERSION AF306566.1 GI:12276059
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 507)
Valentin,E., Singer,A.G., Ghomashchi,F., Lazdunski,M., Gelb,M.H.
and Lambeau,G.

TITLE Cloning and recombinant expression of human group IIF-secreted phospholipase A(2)
JOURNAL Biochem. Biophys. Res. Commun. 279 (1), 223-228 (2000)
MEDLINE 20563827
PUBMED 11112443
REFERENCE 2 (bases 1 to 507)
AUTHORS Valentini, E., Lazdunski, M. and Lambeau, G.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) IPMC, CNRS, 660, Route des Lucioles Sophia Antipolis, Valbonne 06560, France
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Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 481 TCCCGAGCGCCCGCCCGCCCTCCCTAG 507
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AX304469 AX304469 2270 bp DNA linear PAT 30-NOV-2001
LOCUS Sequence 7 from Patent WO0185956.
DEFINITION

AX304469 AX304469.1 GI:17383840
VERSION
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Tribouley, C.M., Yue, H., Khan, F.A., Gandhi, A.R., Au-Young, J., Lal, P., Kearney, L., Elliott, V.S., Ding, L. and Thornton, M.
TITLE Lipid metabolism enzymes
JOURNAL Patent: WO 0185956-A 7 15-NOV-2001;
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Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 282 AGCGTCTCAACTGAAGGCCATGTGGAGCGCGTCACAGGAGGAGCGCCATCTCTGCC 341
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QY 301 CTCACAAAGACAGAGTGTGACAGAGACATCATGTGTGACAAAGACATGTTCTGTGC 360
Db 522 CTCACAAAGACAGAGTGTGACAGAGACATCATGTGTGACAAAGACATGTTCTGTGC 581
QY 361 CTCATGAACACAGAGTGTGACAGAGAGTACCGTGGCTTCTCAATGTCTTACTGCCAGGCG 420
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QY 421 CCCACGCCCAACTGACAGATCTATGAACCGCCCTTGAGGAGGTACCTGCAGTCAACCAA 480
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Db 702 TCCCGAGCGCCCGCCCGCCCTCCCTAG 728
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AK093645 AK093645 2716 bp mRNA linear PRI 15-JUL-2002
LOCUS Homo sapiens cDNA FLJ36326 fis, clone THYMU2005576, moderately similar to Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA.
DEFINITION
ACCESSION AK093645
VERSION AK093645.1 GI:21752561
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens thymus cDNA to mRNA, clone LIB:THYMU2

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clone:THYMU2005576.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H.,
Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A.,
Kavakani,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuho,Y., Nagai,K.
and Isogai,T.
TITLE NED0 human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2716)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NED0 human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
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DB 412 GACTGTGTGGCCACCGCCAGCTGCTCTACCGAGCACTCTTTGACCAAGGCTGTCCAC 471
QY 241 CCTATGTGGCACTATATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 300
DB 472 CCTATGTGGCACTATGATCACACCATCGAGACACACTGAGATAGTCTGCAGTGAC 531

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QY 301 CTCACAAGACAGAGTGTGACAGCAGACATGCATGTGTGACAAGAACATGTTCTGTGC 360
DB 532 CTCACAAGACAGAGTGTGACAGCAGACATGCATGTGTGACAAGAACATGTTCTGTGC 591
QY 361 CTCATGAACACAGAGTGTGACAGCAGAGGAGTACCGTGGCTTCCCTCAATGTCTACTGCCAGGC 420
DB 592 CTCATGAACACAGAGTGTGACAGCAGAGGAGTACCGTGGCTTCCCTCAATGTCTACTGCCAGGC 651
QY 421 CCCACGCCCAACTGCAGCATCTATGAACGCCGCCCTGAGGAGTACCTGCAGTCCACCA 480
DB 652 CCCACGCCCAACTGCAGCATCTATGAACGCCGCCCTGAGGAGTACCTGCAGTCCACCA 711
QY 481 TCCCAGCGCCGCCGCCCTGCCCTAG 507
DB 712 TCCCAGCGCCGCCGCCCTGCCCTAG 738
RESULT 4
LOCUS AF166099 906 bp mRNA linear ROD 02-NOV-1999
DEFINITION Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA,
complete cds.
ACCESSION AF166099
VERSION AF166099
KEYWORDS AF166099.2 GI:6174880
SOURCE Mus musculus.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 906)
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
On the diversity of secreted phospholipases A(2). Cloning, tissue
distribution, and functional expression of two novel mouse group II
enzymes
J. Biol. Chem. 274 (44), 31195-31202 (1999)
20002639
10531313
2 (bases 1 to 906)
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
Direct Submission
Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
3 (bases 1 to 906)
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
Direct Submission
Submitted (02-NOV-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
Sequence update by submitter
On Nov 2, 1999 this sequence version replaced gi:6164699.
REMARK Location/Qualifiers
FEATURES
source
1..906
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
1..906
/gene="Pla2g2f"
251..757
/gene="Pla2g2f"
/EC_number="3.1.1.4"
/notes="Ca2+-dependent secreted phospholipase A2"
/codon_start=1
/product="group IIF secreted phospholipase A2"
/protein_id="AF04500.2"
/db_xref="GI:6174881"
/translation="MKKFFAIVLAGSVVTTAHSLLNLSKMSVEATHRNLSISFVGY
GCYCGIGGRGHPMDVDMCHADCCYKELFEGCRPYVDHYDHTIENITVICTELN
ETECQKQTCEDCKSLTLCKDHPYRNRYGVFNVCQPTNCSLYDPYEEVTCGHG
LPATPVST"
BASE COUNT 208 a 265 c 256 g 177 t
ORIGIN
Query Match 67.2%; Score 340.6; DB 10; Length 906;
Best Local Similarity 79.5%; Pred. No. 3.3e-66;

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Matches	403;	Conservative	0;	Mismatches	104;	Indels	0;	Gaps	0;
QY	1	ATCAAGAAGTCTTCAACCGTGGCCATCTTGTCTGGCAGCGTCTTGTCCACAGCTCAACGCG	60						
Db	251	ATGAAGAATTTCTTGGCATCCGAGTCTCTGGCGGAGTGTGTAAACACGCGCCACAGC	310						
QY	61	AGCGTGTCAACCTGAAGCGCATGTGGAGCGGTGCACAGGAGGAGCGCCATCTGTCC	120						
Db	311	AGCCTGTGAACCTTGAAGTCCATGTGTGGAGCCATCACCACAGAAATCCATCTCTGTC	370						
QY	121	TTGTGGCTACCGTTCTTCACTGTGGTGGGCGCGTGGCCAGCCCAAGGATGAGGTG	180						
Db	371	TTTGTGGCTACCGTCTTCACTGTGGTGGGCGCGTGGCCAGCCCAAGGATGAGGTG	430						
QY	181	GACTGTGCTGCCACGCCACGACTGTCTACCAAGAACTCTTTGACCAAGCTGTCTAC	240						
Db	431	GACTGTGCTGCCACGCCACGACTGTCTATGAGAAGCTCTTTGAGCAGGCGTCCGC	490						
QY	241	CCCTATGTGACCACTATGATACACCATCGAGAACACACACTGAGATGCTCACTGAC	300						
Db	491	CCCTATGTGACCACTATGATACACCATCGAGAACACACACTGAGATGCTCACTGAC	550						
QY	301	CTCAACAGCAGAGTGTGACAGCAGACATGATGTGTGACAGAACATGTTCTGTGC	360						
Db	551	CTCAACAGCAGAGTGTGACAGCAGACATGATGTGTGACAGAACATGTTCTGTGC	610						
QY	361	CTCATGACCAACGAGTACCGAGAGGAGTACCGTGGTCTCTCAATGCTCACTGCCAGGC	420						
Db	611	CTCATGACCAACGAGTACCGAGAGGAGTACCGTGGTCTCTCAATGCTCACTGCCAGGC	670						
QY	421	CCAGCGCCACTGACGACTATGACCGCGCCCTGAGGAGTCACTGACGTCACCAA	480						
Db	671	CCAGCGCCACTGACGACTATGACCGCGCCCTGAGGAGTCACTGACGTCACCAA	730						
QY	481	TCCACGCGCCCGCCCGCCCTCCCTAG	507						
Db	731	CTCCCTGCGACCCCTGTCTCAACCTAG	757						
RESULT	5								
LOCUS	HS340N1								
DEFINITION	Human DNA sequence from clone RP3-340N1 on chromosome 1p35-36.2								
	Contains the 3' part of a gene for a novel phospholipase similar to								
	mouse phospholipase A2 group IIF (PLA2G2F), complete sequence.								
ACCESSION	Z98257								
VERSION	298257.1								
KEYWORDS	HTG; phospholipase; PLA2G2F.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 135571)								
AUTHORS	Bird,C.								
TITLE	Direct Submission								
JOURNAL	Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,								
	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk								
	requests: clonerequest@sanger.ac.uk								
COMMENT	On Mar 12, 1998 this sequence version replaced gi:2578090.								
	During sequence assembly data is compared from overlapping clones.								
	Where differences are found these are annotated as variations								
	together with a note of the overlapping clone name. Note that the								
	variation annotation may not be found in the sequence submission								
	corresponding to the overlapping clone, as we submit sequences with								
	only a small overlap as described above.								
	This sequence has been finished according to sequence map criteria								
	as follows. An attempt is made to resolve all sequencing problems,								
	such as compressions and repeats, but not necessarily within known								
	annotated human repeat sequence elements (e.g. Alu). Where the								
	sequence is ambiguous, there is an annotation using the 'unsure'								
	feature key.								
	The following abbreviations are used to associate primary accession								
	numbers given in the feature table with their source databases:								

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> RP3-340N1 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP3-340N1 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-745E8 is at 135468 in this sequence.

FEATURES

source

Location/Qualifiers
1..135571
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p35-36.2"
/clone="RP3-340N1"
/clone_lib="RPCI-3"

repeat_region

1..77
/note="Alu repeat: matches 2..78 of consensus"
2689..2900

gene

/gene="dJ340N1.1"

CDS

/gene="dJ340N1.1"
/note="continues in dJ169023 (AL158172), gene dJ169023.4
match: cDNAs: Em:AF166099"

/codon_start=3

/evidence="not_experimental"
/product="dJ340N1.1 (novel phospholipase similar to mouse phospholipase A2 group IIF (PLA2G2F))"

/protein_id="CAC13707.1"

/db_xref="GI:10697037"

/translation="DLNTECDKOTCMCDKNWVLCMLQNTYREEVGRFLNYCQGP
NCSIYPPPEEVTCSHQSPAPPAP"

misc_feature

/note="match: GSS: Em:B90571"

/complement(3643..4002)

/note="match: GSS: Em:AQ085265"

3755..3942

/note="2 copies 94 mer 95% conserved"

4003..4078

/note="2 copies 38 mer 89% conserved"

6385..6791

/note="match: GSS: Em:AQ007442"

8456..8587

/note="LRR2 repeat: matches 1..125 of consensus"

8636..8819

/note="LRR2 repeat: matches 266..448 of consensus"

8821..11315

/note="HERVE repeat: matches 1..2512 of consensus"

11316..14480

/note="HERVE repeat: matches 2686..5822 of consensus"

14511..14601

/note="HERVE repeat: matches 5915..6005 of consensus"

14661..14727

/note="Harlequin repeat: matches 6829..6895 of consensus"

14731..14896

/note="LRR2 repeat: matches 5..160 of consensus"

14893..15012

/note="LRR2 repeat: matches 266..384 of consensus"

15013..15109

/note="LRR2 repeat: matches 353..449 of consensus"

complement(16791..17143)

/note="match: GSS: Em:AQ279224"

18790..18933

/note="9 copies 16 mer 72% conserved"

18791..18936

/note="73 copies 2 mer gt 74% conserved"

```

repeat_region 18810..18923
/Note="3 copies 38 mer 77% conserved"
repeat_region 20154..20297
/Note="9 copies 16 mer 72% conserved"
repeat_region 20297..20340
/Note="22 copies 2 mer tg 81% conserved"
misc_feature 25520..25869
/Note="match: GSS: Em:AQ225965"
misc_feature 25529..25754
/Note="match: GSS: Em:B58996"
repeat_region 29107..29271
/Note="MER45 repeat: matches 1..178 of consensus"
repeat_region 29272..29333
/Note="MER45B repeat: matches 975..1039 of consensus"
repeat_region 30193..30260
/Note="L1MC/D repeat: matches 5706..5775 of consensus"
misc_feature complement(31785..32194)
/Note="match: GSS: Em:AQ277413"
misc_feature 32909..33153
/Note="match: GSS: Em:B15515"
repeat_region 33499..33681
/Note="LTR16A repeat: matches 121..295 of consensus"
repeat_region 33695..33870
/Note="11 copies 16 mer 64% conserved"
repeat_region 33705..33894
/Note="5 copies 38 mer 66% conserved"
repeat_region 33712..33867
/Note="78 copies 2 mer tg 64% conserved"
repeat_region 33898..34201
/Note="8 copies 38 mer 60% conserved"
repeat_region 33991..34194
/Note="102 copies 2 mer tg 62% conserved"
repeat_region 33998..34205
/Note="13 copies 16 mer 66% conserved"
repeat_region 34208..34321
/Note="57 copies 2 mer tg 69% conserved"
repeat_region 34235..34330
/Note="6 copies 16 mer 71% conserved"
repeat_region 36684..37082
/Note="MER7A repeat: matches 1..346 of consensus"
misc_feature 38387..38773
/Note="match: STS: Em:HS3432A9"
misc_feature 38387..38685
/Note="match: STS: Em:Z51469"
repeat_region 38691..38726
/Note="18 copies 2 mer ca 97% conserved"
misc_feature join(38780..39119,40855..40926)
/Note="match: STS: Em:Aa479352"
misc_feature 40367..40803
/Note="CpG island"
/Note="evidence-not_experimental"
repeat_region 44473..44664
/Note="MER58 repeat: matches 1..198 of consensus"
misc_feature complement(45904..46320)
/Note="match: STS: Em:AA394141"
misc_feature complement(45950..46366)
/Note="match: STS: Em:T86344"
misc_feature complement(46154..46576)
/Note="match: GSS: Em:AQ340310"
misc_feature complement(48597..49196)
/Note="match: STS: Em:AA135547"
repeat_region 52724..53004
/Note="L1MC1 repeat: matches 5600..5876 of consensus"
repeat_region 61040..61202
/Note="FRAM repeat: matches 2..162 of consensus"
repeat_region 63305..63419
/Note="FLAMC repeat: matches 2..119 of consensus"
repeat_region 67470..67491
/Note="11 copies 2 mer aa 100% conserved"
repeat_region 82874..83099
/Note="LTR16A repeat: matches 214..443 of consensus"
repeat_region 86860..87858
/Note="MER11A repeat: matches 1..1266 of consensus"

repeat_region 91919..92837
/Note="MER49 repeat: matches 7..923 of consensus"
repeat_region 93468..93679
/Note="MER4B repeat: matches 3..175 of consensus"
repeat_region 93975..94012
/Note="MER4B repeat: matches 175..212 of consensus"
repeat_region 94013..94077
/Note="MER4D repeat: matches 388..451 of consensus"
repeat_region 94377..94937
/Note="MER4D repeat: matches 451..1015 of consensus"
repeat_region 98792..98904
/Note="MER81 repeat: matches 1..114 of consensus"
repeat_region 99914..100001
/Note="MSTD repeat: matches 313..394 of consensus"
repeat_region 100002..100283
/Note="MSTC repeat: matches 1..317 of consensus"
repeat_region 102743..103070
/Note="MER41A repeat: matches 1..328 of consensus"
repeat_region 103071..103258
/Note="L1PA7 repeat: matches 5960..6141 of consensus"
repeat_region 103288..103525
/Note="MER41A repeat: matches 316..554 of consensus"

Query Match 41.8% Score 212; DB 9; Length 135571;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 GTGACCTCAACAGACAGAGTGTGACAGACAGACATCATGTGTGACAGACATGGTTC 355
Db 2689 GTGACCTCAACAGACAGAGTGTGACAGACAGACATCATGTGTGACAGACATGGTTC 2748
Qy 356 TGTGCTCATGACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 415
Db 2749 TGTGCTCATGACACAGACAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 2808
Qy 416 AGGGCCCAACGCCCACTGACAGCATCTATGAACGCCGCCCTGAGGAGGTACACGTGCAGTC 475
Db 2809 AGGGCCCAACGCCCACTGACAGCATCTATGAACGCCGCCCTGAGGAGGTACACGTGCAGTC 2868
Qy 476 ACCAATCCCGAGCGCCCGCCCGCCCTCCCTAG 507
Db 2869 ACCAATCCCGAGCGCCCGCCCGCCCTCCCTAG 2900

RESULT 6
LOCUS AL158172
DEFINITION Human DNA sequence from clone Rpl-169023 on chromosome 1 Contains ESTs, STSs and GSSs. Contains the PLA2G5 gene for two isoforms of phospholipase A2 group V, a novel gene, the PLA2G2D gene for phospholipase 2 group IID and the 5' part of the gene for a novel phospholipase similar to mouse phospholipase A2 group IIF (PLA2G2F), complete sequence.
ACCESSION AL158172
VERSION AL158172.5 GI:9801324
KEYWORDS HTG: phospholipase; PLA2G2D; PLA2G2F; PLA2G5.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98743)
Wallis J.
Direct Submission
Submitted (25-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 14, 2000 this sequence version replaced gi:9714699.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

```

Mon Feb 10 11:35:45 2003

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

RP1-169023 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pcYPAC2

IMPORTANT: This sequence is not the entire insert of clone

RP1-169023 it may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.

The true left end of clone RP1-169023 is at 1 in this sequence. The

true left end of clone RP3-340M1 is at 98644 in this sequence.

FEATURES

source

1. .98743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP1-169023"
/clone_lib="RPCI-1"
107. .371
/note="match: GSS: Em:B75013"
complement(249. .658)
/note="match: STS: Em:G50772
match: GSS: Em:AQ201252"
630. .756
/note="MER83-internal repeat: matches 1668. .1825 of consensus"
/note="MER65-internal repeat: matches 1665. .1801 of consensus"
928. .1655
/note="MER4-internal repeat: matches 1764. .2472 of consensus"
1636. .1896
/note="LTR8 repeat: matches 1. .257 of consensus"
1897. .2592
/note="MER4-internal repeat: matches 2472. .3484 of consensus"
2593. .2950
/note="THE1B repeat: matches 1. .364 of consensus"
2951. .3152
/note="MER4-internal repeat: matches 3484. .3679 of consensus"
3157. .5261
/note="MER4-internal repeat: matches 3840. .6087 of consensus"
5262. .5337
/note="AluY repeat: matches 228. .303 of consensus"
5338. .5858
/note="MER4-internal repeat: matches 6087. .6596 of consensus"
5865. .6336
/note="MER42 repeat: matches 1. .504 of consensus"
6337. .6694
/note="L1MC4 repeat: matches 6189. .6548 of consensus"
6897. .7044
/note="L1MC2 repeat: matches 6050. .6202 of consensus"
7063. .7122
/note="MLT1E repeat: matches 507. .567 of consensus"
7800. .8099
/note="L1M4 repeat: matches 5497. .5798 of consensus"

misc_feature

misc_feature

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

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misc_feature

misc_feature

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repeat_region

repeat_region

repeat_region

repeat_region

gene

mRNA

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

CDS

repeat_region

repeat_region

misc_feature

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

complement(7990. .8417)

/note="match: GSS: Em:AQ263839"

complement(8044. .8537)

/note="match: GSS: Em:AQ591805"

8198. .8361

/note="L2 repeat: matches 2537. .2705 of consensus"

8984. .9131

/note="L2 repeat: matches 2414. .2576 of consensus"

9244. .9359

/note="L1MC1 repeat: matches 6210. .6327 of consensus"

9376. .9483

/note="LIP13 repeat: matches -651. .-544 of consensus"

9520. .10539

/note="L1M4 repeat: matches 2963. .3988 of consensus"

10553. .10664

/note="L1M4 repeat: matches 2243. .2357 of consensus"

10655. .10936

/note="AluSx repeat: matches 5. .276 of consensus"

10937. .10951

/note="L1M4 repeat: matches 2230. .2244 of consensus"

10939. .11702

/note="L1M4C repeat: matches 2206. .2980 of consensus"

12233. .12282

/note="AluSx repeat: matches 251. .302 of consensus"

12293. .12588

/note="AluJo repeat: matches 1. .306 of consensus"

join(12774. .12834,16626. .16744,22015. .22080,44003. .44308)

/gene="dJ169023.2"

join(<12774. .12834,16626. .16744,22015. .22080,44003. .44308)

/gene="dJ169023.2"

/product="dJ169023.2.1 (novel protein)"

/note="match: ESTs: Em:AA402475 Em:AA293827"

/evidence="not_experimental"

13384. .13694

/note="AluSx repeat: matches 1. .312 of consensus"

13868. .14158

/note="AluSp repeat: matches 1. .309 of consensus"

14447. .14752

/note="AluJb repeat: matches 3. .307 of consensus"

15010. .15387

/note="MSTA repeat: matches 1. .426 of consensus"

15654. .15790

/note="AluJo repeat: matches 1. .133 of consensus"

16192. .16348

/note="AluJo repeat: matches 137. .296 of consensus"

join(16736. .16744,22015. .22080,44003. .44032)

/gene="dJ169023.2"

/note="5' UTR probably continues in BA66M4 (AL360079)

3rd exon misses correct 3' splice site"

/codon_start=1

/evidence="not_experimental"

/product="dJ169023.2.1 (novel protein)"

/protein_id="CAC13157.1"

/db_xref="GI:10862734"

/translation="MSMPLIQEGTHSPSPPTQQSQSDSGHRTW"

17434. .17743

/note="AluSx repeat: matches 1. .309 of consensus"

17754. .17885

/note="FLAM_C repeat: matches 1. .132 of consensus"

complement(17768. .18077)

/note="match: GSS: Em:AQ880240"

17957. .18057

/note="MER5A repeat: matches 10. .109 of consensus"

18254. .18995

/note="L1MC2 repeat: matches 5582. .6328 of consensus"

19004. .19128

/note="FAM repeat: matches 1. .124 of consensus"

19139. .19511

/note="L1MC2 repeat: matches 5204. .5592 of consensus"

19567. .19724

/note="MER63 repeat: matches 1. .783 of consensus"

19867. .20140

/note="AluJo repeat: matches 1. .265 of consensus"


```

misc_feature      88339..107178
/note="assembly_fragment:00095
fragment_chain:2"
misc_feature      107279..159991
/note="assembly_fragment:00877
fragment_chain:2"
misc_feature      160092..175174
/note="assembly_fragment:01936
fragment_chain:2"
misc_feature      175275..186589
/note="assembly_fragment:00819
fragment_chain:2
vector_end:SP6
vector_side:right"
BASE COUNT      47647 a 45898 c 45957 g 45956 t 1131 others
ORIGIN

Query Match      26.8%; Score 135.8; DB 2; Length 186589;
Best Local Similarity 77.7%; Pred. No. 2.1e-20;
Matches 164; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 297 TGACCTCAACAAGACAGAGTGTGACAAAGCAGACATGTCATGACAAAGACATGTTCT 356
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51156 TGAGCTCAATGAGACGAGTGTGACAAAGCAGACATGTCATGACAAAGACATGTTCT 51097
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 357 GTGCCTCATGACACAGCTACCGAGAGGATACCGTGGCTTCTCAATGTTACTGCCA 416
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51096 GTGCCTCAAGATACCATCAGGAGAAAGTACCGAGGCTACTTCAACGTCTACTGCCA 51037
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 417 GGGCCCCACGCCCACTGACGATCTATGAACGCCGCCCTGAGAGGTCACCTGCAGTCA 476
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51036 GGGCCCCACACCCCACTGACGATCTATGACCCGTACCCAGAGAGTCACTGTGGCA 50977
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 477 CCAATGCCAGCGCCCGCCCGCCCTCCCTAG 507
||||| ||||| ||||| ||||| |||||
Db 50976 TGGCGTCCCTCGACCCCTGTCTCAACCTAG 50946

RESULT 8
AC118094
LOCUS      Rattus norvegicus clone CH230-117D17, *** SEQUENCING IN PROGRESS
DEFINITION *** 74 unordered pieces.
ACCESSION AC118094
VERSION AC118094.4 GI:21746730
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 157317)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,K., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Edgarhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., King,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lounseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Ruiz,S., Savary,G., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Roiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sotak,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Sutton,A., Svatek,A., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Tansey,J., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Usmani,K., Vasquez,L., Warren,R., Washington,C., Watlington,S., Wang,S., Ward-Moore,S., Warren,R., Wleczyk,R., Woodson,S., Worley,K., Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUXU
Center clone name: CH230-117D17
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 98821 bases at least Q40
Consensus quality: 107462 bases at least Q30
Consensus quality: 113497 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 74 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. But the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1465 1564: gap of unknown length
* 1565 2729: contig of 1165 bp in length
* 2730 2829: gap of unknown length
* 2830 4337: contig of 1508 bp in length
* 4338 4437: gap of unknown length
* 4438 5750: contig of 1313 bp in length
* 5751 5850: gap of unknown length
* 5851 6936: contig of 1085 bp in length
* 6936 7036: gap of unknown length
* 7036 8821: contig of 1785 bp in length
* 8821 8920: gap of unknown length
* 8921 10000: contig of 1080 bp in length

10001 10100: gap of unknown length
 10101 11437: contig of 1337 bp in length
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 11538 12665: contig of 1128 bp in length
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 43482 44745: contig of 1265 bp in length
 44746 44845: gap of unknown length
 44847 45958: contig of 1112 bp in length
 45959 46058: gap of unknown length
 46059 47650: contig of 1592 bp in length
 47651 47750: gap of unknown length
 47751 49927: contig of 2177 bp in length
 49928 50027: gap of unknown length
 50028 51030: contig of 1003 bp in length
 51031 51130: gap of unknown length
 51131 52206: contig of 1076 bp in length
 52207 52306: gap of unknown length
 52307 54036: contig of 1720 bp in length
 54037 54136: gap of unknown length
 54137 55922: contig of 1796 bp in length
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 61244 61343: gap of unknown length
 61344 63376: contig of 2033 bp in length
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 63477 65063: contig of 1587 bp in length
 65064 65163: gap of unknown length
 65164 66547: contig of 1384 bp in length
 66548 68236: contig of 1589 bp in length
 68237 68336: gap of unknown length
 68337 70070: contig of 1734 bp in length
 70071 70170: gap of unknown length

* 70171 71751: contig of 1581 bp in length
 71752 71851: gap of unknown length
 71852 73903: contig of 2052 bp in length
 73904 74004: gap of unknown length
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 80683 82392: contig of 1710 bp in length
 82393 82492: gap of unknown length
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 84155 86091: contig of 1937 bp in length
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 86192 87837: contig of 1646 bp in length
 87838 87937: gap of unknown length
 87938 91049: contig of 3112 bp in length

Query Match 25.5%; Score 129.4; DB 2; Length 157317;
 Best Local Similarity 75.8%; Pred. No. 5.8e-19;
 Matches 160; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 297 TGACCTCAACAGACAGAGTGTGACAGCAGCATGTCATGTGTGACAGAACATGGTTCT 356
 Db 36476 TGAGCTCAATGAGCCGAGTGTGATAGCAGACGCTGTGATGTGACAGAACCTGACTCT 36535

QY 357 GTGCCTCATGACACGAGCTACCGAGAGGAGTACCGTGGCTTCCTCAATGCTACTGCCCA 416
 Db 36536 GTGCCTCAAGGACCATCGTACAGCGAAAGTACCGAGGTACCTCAATGCTACTGTCA 36595

QY 417 GGGCCCGACGCCCACTGACGATCTATGACCCCGCCCTGAGGAGGTACCTGCGAGTCA 476
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QY 477 CCAATGCCAGCGCCCGCCCGCCCTGCGCTAG 507
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RESULT 9
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 DEFINITION Rattus norvegicus clone CH230-14317, *** SEQUENCING IN PROGRESS
 AC106106
 VERSION AC106106.2 GI:21728835
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 176574)
 Muzny,D.M., Adams,C., Adlo-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
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 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Mon Feb 10 11:35:45 2003

Hernandez, O., Hodson, A., Hognes, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
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Miner, G., Rojas, A., Mitcheil, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okuwonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,
Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, Y., Villaion, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
2 (bases 1 to 176574)
Worley, K.C.

Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 176574)
Worley, K.C.

Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:18138623.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GHJ
Center clone name: CH230-14317
----- Summary Statistics -----
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 121890 bases at least Q40
Consensus quality: 126967 bases at least Q30
Consensus quality: 131259 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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57631: contig of 2407 bp in length
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60252: contig of 2521 bp in length
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62016: contig of 1664 bp in length
62116: gap of unknown length
64838: contig of 2722 bp in length
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Query Match	19.5%;	Score 99;	DB 9; Length 878;
Best Local Similarity	57.2%;	Pred. No. 5.1e-12;	
Matches 202;	Conservative 0;	Mismatches 145;	Indels 6; Gaps 1;
QY	40	GTTCGTCCACAGTCACGGGAGCGTCTCAACCTGAAGGCCATGTGGAGGCCGTGACA	99
Db	68	GGTGTGATTCAATCAATCAGGGGGGATCTCTGAACCTGAACAAAGATGGTCAAGCAAGTGACT	127
QY	100	GGGAGGAGCGCCATCTGCTCTGCTGGGCTACCGTTGCTACTGTGGCTGGGGGCCGT	159
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QY	160	GGCCAGCCCAAGGATGAGGTGGCTGTGGCCACGCCACGACTGCTCTACCAAGGAA	219
Db	188	GGCCAAACCAAGATGCCACGACTGGTGTGTGGCCAGCCATGACTGCTCTATGACCAC	247
QY	220	CNCTTTGACGAGGCTGTACCCCTATGTGGACACATATATACACCATCGAGACAC	279
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QY	280	ACTGAGATAGTCTGCAGTGCACCTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGT	339
Db	302	CAGGGACATCCACTGCTCTGACAAGGAGTGTGTGTGGCAGCAGCTGTGTGCTGT	361
QY	340	GACAAGACATGGTTCTGTGTGCTCATGAACAGACAGTACCGAGAGGATACCG	392
Db	362	GACAAGAGGTGGCTTCTGCTCTGAAGGCAACCTGCACACCTACCAAGAGCG	414
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AF112982			
LOCUS	AF112982	1938 bp	linear
DEFINITION	Homo sapiens phospholipase A2 (SPLASH) mRNA, complete cds.		
ACCESSION	AF112982		
VERSION	AF112982.1	GI:6453792	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1938)		
TITLE	Shakhov.A.N., Rubtsov.A.V., Lyakhov,I.G., Tumanov.A.V. and Nedospasov,S.A.		
JOURNAL	SPLASH (PLA2IID), a novel member of phospholipase A2 family, is associated with lymphotoxin deficiency		
MEDLINE	Genes Immun. 1 (3), 191-199 (2000)		
PUBMED	21040292		
AUTHORS	11196711		
REFERENCE	2 (bases 1 to 1938)		
JOURNAL	Shakhov.A.N., Rubtsov.A.V., Lyakhov,I.G., Tumanov.A.V. and		


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RESULT 13
AX464400
LOCUS      AX464400          496 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 533 from Patent WO0140466.
ACCESSION  AX464400
VERSION     AX464400.1  GI:21899216
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
            same
JOURNAL
FEATURES
source      Genentech Inc. (US)
            Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT  200 a  95 c  104 g  95 t      2 others
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Best Local Similarity 63.5%; Pred. No. 3.1e-11;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
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Db  128 GGGAAATGCCATCTCTCTACTGGCCCTACGGCTGTCACCTGGGACTAGTGGCAGA 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  160 GGGCAGCCCAAGNATAGTGGACTGTGTGTCACGCCACGACGTCGCTGCTACCAAGGAA 219
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Db  188 GGGCAACCCAAAGATGCCAGGACTGTGTGTCAGACACCCATGACTGCTGCTATGACCAC 247
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QY  220 CTCTTTGACCAAGGCTGTACCCCTATGTGACCACTATGATCACACCAT 269
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Db  248 CTGAAGACCCAGGGTGGCGCATCTACAAGGACAAACAAAGACGACAT 297
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RESULT 14
MMU18119
LOCUS      MMU18119          1445 bp      mRNA      linear      ROD 30-MAY-2001
DEFINITION Mus musculus testis-specific low molecular weight phospholipase A2
            mRNA, complete cds.
ACCESSION  U18119
VERSION     U18119.1  GI:1049007
KEYWORDS
SOURCE      Mus musculus.
ORGANISM    Mus musculus
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE       Balboa,M.A., Balsinde,J., Winstead,M.V., Tischfield,J.A. and
            Dennis,E.A.
JOURNAL     Novel group V phospholipase A2 involved in arachidonic acid
            mobilization in murine P388D1 macrophages
MEDLINE     J. Biol. Chem. 271 (50), 32381-32384 (1996)
PUBMED      97113049
AUTHORS     2 (sites)
            Chen,J., Shao,C., Lazar,V., Srivastava,C.H., Lee,W.H. and
            Tischfield,J.A.
TITLE       Localization of group IIC low molecular weight phospholipase A2

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mRNA to meiotic cells in the mouse
J. Cell. Biochem. 64 (3), 369-375 (1997)
97209919
9057094
3 (bases 1 to 1445)
Tischfield,J.A.
Direct Submission
Submitted (05-DEC-1994) Jay A. Tischfield, Medical and Molecular
Genetics, Indiana University School of Medicine, 975 W. Walnut,
Indianapolis, IN 46202, USA
Location/Qualifiers
1..1445
/organism="Mus musculus"
/db_xref="taxon:10090"
179..631
/codon_start=1
/evidence=experimental
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/protein_id="AAC52936.1"
/db_xref="GI:1049008"
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GCYGLGGKGLUPVDATDRCCWAHDCCHLKEYGCPILNAYQFTIVNGTVTCGCTVA
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BASE COUNT  361 a  388 c  384 g  312 t
ORIGIN
Query Match      18.4%; Score 93.2; DB 10; Length 1445;
Best Local Similarity 56.4%; Pred. No. 1e-10;
Matches 195; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
QY  47  CCACAGCTCACGGCAGCGTCTCAACCTGAAGCCCATGTGGAGCGCGTCACAGGAGGA 106
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Db  225  CTTCCACCTCAGCAGATTTCTGGCAGTTCACAGAGATGTCAACACGTTCACAGGCGCA 284
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QY  107 GGGCCATCTGCTCTCTGGCTACGGTTGCTACTGTGGCTGGGGGGCCGTGGCCAGC 166
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Db  285  GCGCTTCTCTCTATTACGGATATGGCTGCTACTGTGGCTTGGGGCAAGGCTCC 344
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  167 CCAAGGATGAGTGAGTGGTGTGCTGCCAGCCGACGACTGCTGCTACCAAGGAATCTTTG 226
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  345  CTGTGGATGCCACAGACAGAGTGTGCTGGGCTCATGCTGTACCAACAGCTTAAGG 404
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QY  227 ACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCATCGAAGAACACTGAGA 286
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Db  465  CCGTGGATGCCACCGTGGCAGCAGCTGCCCTGGGGGAGGAGGCTGTGAGTGTGACA 524
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QY  344  AGAACATGTTCTGTGCTCATGAACACGACGTACCGAGAGGAGTA 389
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Db  525  AACAGTCTGTGCTACTGCTTCAAGGAGAACCTGGCCACCTACGAGAA 570
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RESULT 15
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DEFINITION Mus musculus, Similar to phospholipase A2, group IIC, clone
            MGC:18412 IMAGE:4234596, mRNA, complete cds.
ACCESSION  BC029347
VERSION     BC029347.1  GI:20810357
KEYWORDS    MGC.
SOURCE      house mouse.
ORGANISM    Mus musculus
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE       1 (bases 1 to 1480)
            Strausberg,R.
JOURNAL     Direct Submission
            Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 00:07:54 : Search time 227 Seconds

(without alignments)
5029.794 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	507	100.0	2270	24	ABA96002 Human lipid metabo
2	99	19.5	592	21	AAA53269 Human phospholipas
3	99	19.5	854	22	AAS14884 Human CDNA encodin
4	99	19.5	878	21	AAA60878 Human secretory ph
5	99	19.5	1927	22	AH98759 Human EST-derived
6	99	19.5	1927	22	AAD99768 Human protein enco
7	99	19.5	1931	22	AAD19218 Human CG95 (or C87
8	95.6	18.9	496	21	AAA77684 Human PRO1561 cDNA
9	95.6	18.9	496	22	AAS21510 Human CDNA sequenc

10	95.6	18.9	496	22	AAF54466	DNA encoding prote
11	95.6	18.9	497	21	AAA37132	Human PRO1561 (UNQ
12	86.4	17.0	4325	16	AAQ81136	RPLA2-8 gene. Ra
13	82.8	16.3	1828	16	AAQ81137	RPLA2-10 gene. Ra
14	82.4	16.3	1233	21	AAA72076	cDNA encoding mous
15	82.4	16.3	1233	21	AAA60866	Mouse secretory ph
16	82	16.2	501	21	AAA72077	cDNA fragment enco
17	82	16.2	501	21	AAA60854	Mouse secretory ph
18	76.8	15.1	1014	16	AAQ81138	HPLA2-10 gene. Ho
19	76.8	15.1	1016	24	ABL59517	Human phospholipas
20	75.8	15.0	465	24	ABL58672	Human X-type secre
21	75.8	15.0	465	24	ABA96622	Human X-type secre
22	75.8	15.0	742	20	AA79001	Human phospholipas
23	75.8	15.0	1020	24	ABL58671	Human secretory ph
24	75.8	15.0	1020	24	ABA96621	Human X-type secre
25	75.8	15.0	1737	23	AA591740	DNA encoding novel
26	71.2	14.0	487	22	AA77401	Human phospholipas
27	68.2	13.5	1276	23	AA587642	DNA encoding novel
28	65.8	13.0	445	24	ABL61868	Colon adenocarcino
29	65.8	13.0	445	24	ABL67612	Oesophagus cancer
30	63.8	12.6	1040	24	ABL58680	Mouse X-type secre
31	63.8	12.6	1040	24	ABA96630	Mouse X-type secre
32	61.8	12.2	459	22	AAH42606	Nucleotide sequenc
33	60.8	12.0	518	10	AA91256	DNA sequence of hu
34	60.4	11.9	883	21	AA73130	Mouse secretory ty
35	60.4	11.9	883	22	AA77387	Murine CDNA encodi
36	59.4	11.7	432	14	AAQ48537	Phospholipase A2 c
37	59.4	11.7	470	14	AAQ48538	Phospholipase A2 c
38	57.8	11.4	479	13	AAQ26372	PLA2 CDNA. Synthe
39	57.8	11.4	854	10	AA91258	Nucleotide sequenc
40	57.8	11.4	854	24	ABL69731	Prostate cancer re
41	57.8	11.4	1076	21	AAF15635	Human prostate can
42	57.8	11.4	1116	20	AA241274	Human normal ovari
43	57.4	11.3	456	24	ABL60543	Human lipid metabo
44	57.2	11.3	447	24	ABK47377	Human Phospholipas
45	57.2	11.3	562	21	AAF21222	Human low adenosin

ALIGNMENTS

RESULT 1

ABA96002

ID ABA96002 standard; cDNA; 2270 BP.

XX ABA96002;

AC ABA96002;

DT 04-MAR-2002 (first entry)

XX Human lipid metabolism enzyme-2 (LME-2) CDNA.

DE Human; LME-2; lipid metabolism enzyme-2; cytostatic; neuroprotective; immunosuppressive; anti-inflammatory; cardiovascular; gene therapy; enzyme therapy; cancer; neurological disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 93..728

FT FT /*tag= a

FT FT /product= "LME-2"

XX WO200185956-A2.

PN 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US15210.

XX 11-MAY-2000; 2000US-203511P.

PR 25-MAY-2000; 2000US-207903P.

PR 07-JUN-2000; 2000US-210150P.

PR 23-JUN-2000; 2000US-213392P.

2D NO.7

XX (INCY-) INCYTE GENOMICS INC.
PA Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;
XX WPI; 2002-089794/12.
DR P-PSDB; ABB08202.
XX New lipid metabolism enzymes useful for diagnosing, treating and
PT preventing cancer, neurological disorders, autoimmune/inflammatory
PT disorders, and cardiovascular disorders -
XX
PS Claim 5; Page 118-119; 122pp; English.
XX The sequence encodes a novel human lipid metabolism enzyme (LME-2) of
CC the invention. The invention relates to novel human LME's, and the
CC polynucleotides which identify and encode them. The enzymes of the
CC invention have cytostatic, neuroprotective, immunosuppressive,
CC anti-inflammatory, and cardiovascular activity. The polypeptides and
CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
CC metabolism enzymes are useful in the diagnosis, treatment and prevention
CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
CC cardiovascular disorders, and in the assessment of the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
CC for compounds that modulate the activity of LME. Polynucleotides encoding
CC LME may be used for somatic or germline gene therapy, to detect and
CC quantify gene expression in biopsied tissues in which expression of LME
CC may be correlated with disease, to generate a transcript image of a
CC tissue or cell type, to generate hybridization probes useful in mapping
CC the naturally occurring genomic sequence, and for screening libraries of
CC compounds in drug screening techniques. The polypeptide sequences may be
CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
CC primers derived from polynucleotide sequences encoding LME may be used to
CC detect single nucleotide polymorphisms.
XX
SQ Sequence 2270 BP; 476 A; 690 C; 709 G; 395 T; 0 other;

Query Match 100.0%; Score 507; DB 24; Length 2270;
Best Local Similarity 100.0%; Pred. No. 3.7e-119;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 222 ATGAAGAAGTTCTTACACCGTGGCCATCTTGTGTCAGGCGTTCTTCCACAGCTCACGGC 281
QY 61 AGCTGCTCAACCTGAAGCCATGTGTGGAGCCGTCACAGGAGGAGGCCATCTGTGCC 120
Db 282 AGCTGCTCAACCTGAAGCCATGTGTGGAGCCGTCACAGGAGGAGGCCATCTGTGCC 341
QY 121 TTCGTGGGTACGGTTGCTACTGTGGCTGGGGGCCGTCAGCCCAAGGATCAGGTG 180
Db 342 TTCGTGGGTACGGTTGCTACTGTGGCTGGGGGCCGTCAGCCCAAGGATCAGGTG 401
QY 181 GACTGTGTGTCACGCCGCCACGACTGCTGCTACAGGAACTCTTTGACCAAGGCTGTGCAC 240
Db 402 GACTGTGTGTCACGCCGCCACGACTGCTGCTACAGGAACTCTTTGACCAAGGCTGTGCAC 461
QY 241 CCTATGTGGACACTATGATACACCATCGAGACACACACTGAGATGTGTGACGTGAC 300
Db 462 CCTATGTGGACACTATGATACACCATCGAGACACACACTGAGATGTGTGACGTGAC 521
QY 301 CTCACCAAGCAGAGTGTGACAGCAGACATCATGTGTGACAAACATGTTCTGTGC 360
Db 522 CTCACCAAGCAGAGTGTGACAGCAGACATCATGTGTGACAAACATGTTCTGTGC 581
QY 361 CTCATGAACACGACGTACCGAGGAGGAGTACCGTGGCTTCTCTCAATGTCTACTGCCAGGGC 420
Db 582 CTCATGAACACGACGTACCGAGGAGGAGTACCGTGGCTTCTCTCAATGTCTACTGCCAGGGC 641
QY 421 CCCACGCCCAACTGAGCATCTATGAACGCCGCCCTGAGGAGGTACCTGACGTACCAAA 480

Db 642 CCCACGCCCAACTGAGCATCTATGAACGCCGCCCTGAGGAGGTACCTGACGTACCAAA 701
QY 481 TCCCAGCGCCCGCCCGCCCTCCCTAG 507
Db 702 TCCCAGCGCCCGCCCGCCCTCCCTAG 728
RESULT 2
AAAS3269
ID AAAS3269 standard; cDNA; 592 BP.
XX AC AAAS3269;
XX 05-OCT-2000 (first entry)
XX Human phospholipase 1 HPPL1 coding sequence.
XX Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 29..466
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FT /product= "HPPL1"
FT sig_peptide 29..91
FT /tag= b
FT /note= "this is a putative signal peptide"
FT sig_peptide 29..76
FT /tag= c
FT /note= "this is a putative signal peptide"
FT mat_peptide 77..463
FT /tag= d
FT /note= "this is a putative mature HPPL1"
FT mat_peptide 92..463
FT /tag= e
FT /note= "this is a putative mature HPPL1"
XX
XX WO200024911-A2.
XX
XX 04-MAY-2000.
XX
XX 27-OCT-1999; 99WO-US25021.
XX
XX 27-OCT-1998; 98US-0181317.
PR 21-JAN-1999; 99US-0234726.
XX
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI Azimzai Y, Lal P, Lu DAM;
XX
XX WPI; 2000-350750/30.
DR P-PSDB; AAB03627.
XX
XX Human phospholipase genes and proteins useful to diagnose, prevent or
PT treat cancer, autoimmune or inflammatory or reproductive disorders -
PT
XX Claim 9; Page 74; 80pp; English.
XX
XX The present sequence is the coding sequence of human phospholipase 1
CC (HPPL1). The protein produced from this sequence is involved in the
CC hydrolysis of membrane phospholipids. The protein and its coding sequence
CC can be used to diagnose and treat the following: cancers such as
CC prostate, breast and testicular cancers, autoimmune and inflammatory
CC disorders such as AIDS, allergies, anaemia, asthma, atherosclerosis,
CC Crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable
CC bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis,
CC rheumatoid arthritis and systemic lupus erythematosus, infection caused
CC by viruses, fungi, bacteria, parasites and protozoa, and reproductive
CC disorders including infertility, disruptions of the menstrual cycle,

CC polycystic ovary syndrome, ectopic pregnancies, disruptions of
CC spermatogenesis, cancers within the reproductive tract and impotence.
CC This coding sequence was obtained from clone no.2641779, which was
CC constructed using lung tumour tissue.

XX Sequence 592 BP; 126 A; 182 C; 165 G; 119 T; 0 other;

Query Match 19.5%; Score 99; DB 21; Length 592;
Best Local Similarity 57.2%; Pred. No. 1.3e-15;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCACAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGGTGGAGCCCTGCAC 99
DB 68 GGTGTGATTCACATCCAGGCGGGTCTTGAACCTGACACAGATGGTCAAGCAAGTACT 127
QY 100 GGGAGAGCGCCATCCTGCTTCCTGGGCTACGTTGCTACTGTGGCTGGGGGGCGGT 159
DB 128 GGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGCGACTAGGTGGCAGA 187
QY 160 GCCCAGCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 219
DB 188 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 247
QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCATCGAGAACAC 279
DB 248 CTCAGAGCCCGGGTGGCGGATCTACAGGACTATTACAGATACAACTT-----TTCC 301
QY 280 ACTGAGATAGTGTGAGTGCCTCAACAGACAGAGTGTGACAGACAGATGATGTGT 339
DB 302 CAGGGGAACATCACTGCTGTGACAGGAAGTGTGTGAGCAGAGTGTGTGCTGTGT 361
QY 340 GACAGAAATGTTCTGTGCTCTACGACAGAGCTACCGAGAGAGTACCG 392
DB 362 GACAAGGAGGTGGCTTGTGCTGAGGCGCAACCTGGACACATACCAAGAGCG 414

RESULT 3
AAS14884
ID AAS14884 standard; cDNA; 854 BP.

AC AAS14884;

DT 20-DEC-2001 (first entry)

DE Human cDNA encoding novel human protein NHP #5.

KW Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
KW antiarthritic; cystostatic; antiarteriosclerotic; vulnery;
KW neuroprotective; nootropic; antiparkinsonian;
KW anti-human immunodeficiency virus; antiasthmatic; vasotrophic; cardiant;
KW hypotensive; anorectic; antifertility; neuroleptic; anticonvulsant;
KW antimanic; immunosuppressive; cerebroprotective; antimicrobial;
KW antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
KW immunomodulator; antiseborrheic; dermatological; vasoconstriction;
KW gastrointestinal disorder; cardiovascular disorder; hypertension;
KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW hyperproliferative disorder; pulmonary system disorder;
KW central nervous system disorder; bone disorder;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW panic disorder; learning disability; amytropic lateral sclerosis;
KW psychosis; autism; sleep disorder; immune system disorders;
KW Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW diabetes mellitus; immunologic disorder; asthma; AIDS;
KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW neural system disorder; respiratory disorder; olfactory disorder;
KW wound healing.

OS Homo sapiens.

XX

PH Key Location/Qualifiers
FT CDS 22..459
FT /*tag= a
FT /product= "NHP #5"
XX WO200174896-A1.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001: 2001WO-US10542.
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XX 03-APR-2000: 2000US-194118P.
XX 29-SEP-2000: 2000US-236384P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Moore PA, Nil J, Soppet DR, Coleman TA, Gentz RL, Endress GA;
XX Li Y, Dillon PJ;
XX WPI: 2001-626394/72.
XX P-PSDB: AAU09096.
XX
XX New human proteins, useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cardiovascular
XX disorders, autoimmune disorders and reproductive disorders -
XX
XX Claim 1: Page 294; 318pp; English.
XX
XX The invention relates to novel human proteins (NHP) and the
XX nucleic acids that encode them and antibodies raised against them.
XX The proteins, antibodies and nucleic acids are useful in the diagnosis,
XX prognosis, prevention and/or treatment of diseases and/or disorders
XX involving vasoconstriction, gastrointestinal disorders, cardiovascular
XX disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
XX coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,
XX cachexia, disorders of small intestine, disorders of reproductive system
XX (e.g. male infertility and/or impotence), testicular cancer, lung tumours
XX and other hyperproliferative disorders, disorders of pulmonary system,
XX central nervous system disorders, bone disorders, neurodegenerative
XX diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
XX disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
XX panic disorder, learning disabilities, amytropic lateral sclerosis,
XX psychoses, autism, sleep disorders), immune system disorders (e.g.
XX Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
XX central nervous system disorders (e.g. multiple sclerosis, ischaemic
XX brain injury and/or stroke), infectious diseases, diabetes mellitus,
XX immunological disorders (e.g. asthma, acquired immunodeficient syndrome
XX (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
XX sepsis, acne, psoriasis and lupus erythematosus), neural system
XX disorders, respiratory disorders, olfactory disorders and wound
XX healing. The present sequence encodes an NHP of the invention.
XX
SQ Sequence 854 BP; 186 A; 254 C; 238 G; 176 T; 0 other;
Query Match 19.5%; Score 99; DB 22; Length 854;
Best Local Similarity 57.2%; Pred. No. 1.4e-15;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;
QY 40 GTTCTGTCACAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGGTGGAGCCGTGCACA 99
DB 61 GGTGTGATTCACATCCAGGCGGGTACTCTGAACCTGAACAGATGGTCAAGCAAGTACT 120
QY 100 GGGAGGAGCGCCATCTCTCTGCTGGGCTACGGTTGCTACTGTGGCTGGGGGGCGGT 159
DB 121 GGGAAATGCCCATCTCTCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGGTGGCAGA 180
QY 160 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 219
DB 181 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCATCGAGAACAC 279
DB 241 CTGAGAGCCCGGGGTGCAGCATCTACAGGACTATTACAGATACAACTT-----TTCC 294

CC of the invention.

XX
SQ Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 other;
Query Match 19.5%; Score 99; DB 22; Length 1927;
Best Local Similarity 57.2%; Pred. No. 1.8e-15;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCATGCTGGAGCGCGTCACA 99
DB 57 GGTGTGATTCATCCATCCAGCGCGGATCTCTGAACCTGAACAAGATGCTCAAGCAAGTGACT 116
QY 100 GGGAGAGCGCCATCTGTCCTTCCTGGGCTACGGTTCTGCTACTGCTGGGCTGGGCGCGT 159
DB 117 GGGAAATGCCATCTCTCTCTACTGCGCCCTAGGCTGCTCACTGGGACTAGTGGGAGA 176
QY 160 GCCAGCCCAAGGATGAGTGACGTGCTGCTGCCAGCCAGCAGCTGCTGCACCAAGAA 219
DB 177 GGCACCAACCAAGATGCCAGCGAGTGGTGTGCCAGACCCATGACTGCTGCTATGACCAC 236
QY 220 CTCCTTTGACCAAGGCTGTCACCCCTATGCTGGACCACTATGATCACCACCTCGAACAAC 279
DB 237 CTGAAGACCCAGGGTGGCGCATCTACAAGCACTATTACAGATACAACCTT-----TTCC 290
QY 280 ACTGATAGTGTGCGTGAAGCTCAACAGAGAGTGTGACAGCAGATGTCATGTCATGT 339
DB 291 CAGGGGAACATCCACTGCTCTGACAAAGGAAAGTGGTGTGAGCAGCAGCTGTGTCCTGT 350
QY 340 GACAAAGACATGGTTCCTGCTCATGACCAAGCAGACGCTACCGAGAGGAGTACCG 392
DB 351 GACAGGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAGCG 403

RESULT 6

AAH99768
ID AAH99768 standard; cDNA; 1927 BP.

XX

AC AAH99768;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:603.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiac; central nervous system; viricide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antistatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.

OS Homo sapiens.

XX

PN W0200153455-A2.

XX

PD 26-JUL-2001.

XX

PF 22-DEC-2000; 2000WO-US35017.

XX

PR 23-DEC-1999; 99US-0471275.

XX

PR 21-JAN-2000; 2000US-0488725.

XX

PR 25-APR-2000; 2000US-0552317.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

DR P-PSDB; AAM25827.

XX

PT Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX

XX Claim 1; Page 636; 1217pp; English.

XX

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to

XX AAM25963. The proteins can have activities based on the tissues and

XX cells they are expressed in, such as: antinflammatory; antirheumatic;

XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;

XX central nervous system; viricide; anti-HIV; fungicide; antimutagen;

XX cardiovascular; antianaemic; antiaagregant; haemostatic; vulnery;

XX antiulcer; osteopathic; dermatological; antiallergic; antistatic;

XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;

XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides

XX encoding them can be used in gene therapy, antisense therapy and vaccine

XX production. The proteins and polynucleotides are useful for screening for

XX agonists or antagonists of a protein and for the treatment and diagnosis

XX of disorders associated with the activity of a protein e.g. inflammation,

XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,

XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal

XX infections, autoimmunity, genetic diseases, haematopoietic disorders,

XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,

XX osteoporosis, severe combined immunodeficiency, eczema, allergic

XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,

XX Alzheimer's disease, Parkinson's disease, neurodegenerative and

XX neurological disorders.

XX

SQ Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 other;

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		Matches	202;	Conservative	0;	Mismatches	145;	Indels	6;	Gaps	1;
Qy	40	GTTCGTCCACAGCTCAGGCGAGCTGCTCAACCTGAAGCCATGTGGAGGCGGTGACCA	99								
Db	57	GGTGTGATTCACATCCAGGGGGGATCTGAACTGACACAGATGGTCAAGCAAGTGACT	116								
Qy	100	GGGAGGAGCGCCATCTCTGCTGCTGGGCTACGCTTGTGCTTGTGCTGCTGCTGCTGCT	159								
Db	117	GGGAAATGCCATCTCTGCTGCTGGGCTACGCTTGTGCTTGTGCTGCTGCTGCTGCT	176								
Qy	160	GGCCAGCCCAAGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	219								
Db	177	GGCCAAACCAAGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	236								
Qy	220	CTCTTTGACCAAGGCTGTCACCCCTATGTCGACCACTATGATACACCATCGAGAACAAC	279								
Db	237	CTGAAGACCCAGGCTGGGCTATCTACAAAGGACTATTACAGATACAACTT-----TTCC	290								
Qy	280	ACTGAGATAGTTCGAGTGACCTCAACAAAGACAGAGTGTGACAGCAGACATGATGTGT	339								
Db	291	CAGGGGAACATCCACTGCTCTGACAAAGGAAAGCTGGTGTGAGCAGCAGCTGTGTGCTGT	350								
Qy	340	GACAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	392								
Db	351	GACAAGGAGGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	403								
RESULT 8											
AAAT77684											
ID AAA77684 standard; cdna; 496 BP.											
AC AAA77684;											
XX 07-NOV-2000 (first entry)											
DE Human PRO1561 cdna sequence SEQ ID NO:221.											
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;											
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;											
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;											
KW cytostatic; gene therapy; vaccine; ss.											
XX Homo sapiens.											
OS WO200032221-A2.											
PN 08-JUN-2000.											
PD 30-NOV-1999; 99WO-US28313.											
XX 01-DEC-1998; 98WO-US25108.											
XX 16-DEC-1998; 98US-0112850.											
XX 12-JAN-1999; 99WO-US05028.											
XX 08-MAR-1999; 99US-0123957.											
XX 12-MAR-1999; 99US-0131445.											
XX 28-APR-1999; 99US-0134287.											
XX 14-MAY-1999; 99WO-US12252.											
XX 02-JUN-1999; 99US-0141037.											
XX 23-JUN-1999; 99US-0144758.											
XX 26-JUL-1999; 99US-0145698.											
XX 01-SEP-1999; 99WO-US20111.											
XX 08-SEP-1999; 99WO-US20594.											
XX 13-SEP-1999; 99WO-US20944.											
XX 15-SEP-1999; 99WO-US21090.											
XX 15-SEP-1999; 99WO-US21547.											
XX 05-OCT-1999; 99WO-US23089.											
XX 29-OCT-1999; 99US-0162506.											
XX (GETH) GENENTECH INC.											
PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;											
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;											
PI											

Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antilipemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 18..455
/tag= a
/product= "Human CG95 (or C870) lipase protein"
FT 18..89
/tag= b
FT sig_peptide
FT 90..452
/tag= c
FT mat_peptide
/product= "Human mature CG95 (or C870) protein"
XX WO200179446-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US12529.
XX 14-APR-2000; 2000US-197137P.
XX 20-JUN-2000; 2000US-0598042.
XX 03-AUG-2000; 2000US-0631451.
XX 22-SEP-2000; 2000US-0667298.
XX 17-NOV-2000; 2000US-0714936.
XX (HYSE-) HYSEQ INC.
XX Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
XX Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
XX Wang D;
XX WPT; 2001-611724/70.
XX P-PSDB; AAE11924.
XX Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
XX receptor polypeptides, useful for preventing diagnosing and treating
XX lipid metabolism disorders, thrombosis and cardiovascular diseases -
XX Claim 1; Page 153-154; 266pp; English.
XX The invention relates to polynucleotides encoding proteins CG122, CG179,
XX CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
XX involved in lipid metabolism and cardiovascular disease such as human
XX apolipoproteins, lipases and lipoprotein receptor proteins. These DNA
XX and protein sequences are useful for treating or preventing disorders
XX associated with apolipoproteins, lipases and lipoprotein receptor (ALLr)
XX expression and for treating lipid metabolism, cardiovascular diseases
XX and thrombosis. Antibodies against these proteins are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of these sequences. ALLr polypeptides are also
XX useful for identifying agents (agonists and antagonists) that bind to
XX them and cells expressing ALLr proteins are useful for identifying a
XX therapeutic agent for use in treatment of a pathology related to
XX aberrant expression or physiological interactions of this polypeptide.
XX Vectors comprising these DNA and protein sequences are also useful for
XX producing ALLr proteins. The nucleic acids and polypeptides of the
XX invention are also useful for the treatment of occlusive cardiovascular
XX diseases, myocardial infarction, cerebral ischaemia, angina, arterial
XX thrombosis, coronary artery thrombosis and cerebral artery thrombosis
XX or intracardiac thrombosis and stroke. The nucleotides of the invention
XX are used in gene therapy. The present sequence is human CG95 (or C870)
XX lipase DNA.
XX Sequence 1931 BP; 417 A; 600 C; 479 G; 435 T; 0 other;
XX Query Match 19.5%; Score 99; DB 22; Length 1931;
XX Best Local Similarity 57.2%; Pred. No. 1.8e-15;

PR 18-SEP-1998; 98US-0100848.
 PR 18-SEP-1998; 98US-0100849.
 PR 18-SEP-1998; 98US-0101014.
 PR 18-SEP-1998; 98US-0101068.
 PR 22-SEP-1998; 98US-0101071.
 PR 23-SEP-1998; 98US-0101279.
 PR 23-SEP-1998; 98US-0101471.
 PR 23-SEP-1998; 98US-0101472.
 PR 23-SEP-1998; 98US-0101474.
 PR 23-SEP-1998; 98US-0101475.
 PR 23-SEP-1998; 98US-0101476.
 PR 23-SEP-1998; 98US-0101477.
 PR 23-SEP-1998; 98US-0101478.
 PR 24-SEP-1998; 98US-0101738.
 PR 24-SEP-1998; 98US-0101743.
 PR 24-SEP-1998; 98US-0101915.
 PR 24-SEP-1998; 98US-0101916.
 PR 29-SEP-1998; 98US-0102207.
 PR 29-SEP-1998; 98US-0102240.
 PR 29-SEP-1998; 98US-0102307.
 PR 29-SEP-1998; 98US-0102330.
 PR 29-SEP-1998; 98US-0102331.
 PR 30-SEP-1998; 98US-0102484.
 PR 30-SEP-1998; 98US-0102487.
 PR 30-SEP-1998; 98US-0102570.
 PR 30-SEP-1998; 98US-0102571.
 PR 01-OCT-1998; 98US-0102684.
 PR 01-OCT-1998; 98US-0102687.
 PR 02-OCT-1998; 98US-0102965.
 PR 06-OCT-1998; 98US-0103238.
 PR 06-OCT-1998; 98US-0103449.
 PR 07-OCT-1998; 98US-0103314.
 PR 07-OCT-1998; 98US-0103315.
 PR 07-OCT-1998; 98US-0103328.
 PR 07-OCT-1998; 98US-0103395.
 PR 07-OCT-1998; 98US-0103396.
 PR 07-OCT-1998; 98US-0103401.
 PR 08-OCT-1998; 98US-0103633.
 PR 08-OCT-1998; 98US-0103678.
 PR 08-OCT-1998; 98US-0103679.
 PR 14-OCT-1998; 98US-0104257.
 PR 20-OCT-1998; 98US-0104987.
 PR 20-OCT-1998; 98US-0105000.
 PR 21-OCT-1998; 98US-0105002.
 PR 22-OCT-1998; 98US-0105169.
 PR 26-OCT-1998; 98US-0105266.
 PR 26-OCT-1998; 98US-0105693.
 PR 26-OCT-1998; 98US-0105694.
 PR 27-OCT-1998; 98US-0105807.
 PR 27-OCT-1998; 98US-0105881.
 PR 27-OCT-1998; 98US-0105882.
 PR 28-OCT-1998; 98US-0106062.
 PR 28-OCT-1998; 98US-0106023.
 PR 28-OCT-1998; 98US-0106029.
 PR 28-OCT-1998; 98US-0106030.
 PR 28-OCT-1998; 98US-0106032.
 PR 28-OCT-1998; 98US-0106033.
 PR 29-OCT-1998; 98US-0106178.
 PR 29-OCT-1998; 98US-0106248.
 PR 29-OCT-1998; 98US-0106384.
 PR 30-OCT-1998; 98US-0106500.
 PR 30-OCT-1998; 98US-0106464.
 PR 03-NOV-1998; 98US-0106856.
 PR 03-NOV-1998; 98US-0106902.
 PR 03-NOV-1998; 98US-0106905.
 PR 03-NOV-1998; 98US-0106919.
 PR 03-NOV-1998; 98US-0106932.
 PR 10-NOV-1998; 98US-0106934.
 PR 17-NOV-1998; 98US-0107783.
 PR 17-NOV-1998; 98US-0108775.

PR 17-NOV-1998; 98US-0108779.
 PR 17-NOV-1998; 98US-0108787.
 PR 17-NOV-1998; 98US-0108788.
 PR 17-NOV-1998; 98US-0108801.
 PR 17-NOV-1998; 98US-0108802.
 PR 17-NOV-1998; 98US-0108806.
 PR 17-NOV-1998; 98US-0108807.
 PR 17-NOV-1998; 98US-0108867.
 PR 18-NOV-1998; 98US-0108925.
 PR 18-NOV-1998; 98US-0108848.
 PR 18-NOV-1998; 98US-0108849.
 PR 18-NOV-1998; 98US-0108850.
 PR 18-NOV-1998; 98US-0108851.
 PR 18-NOV-1998; 98US-0108852.
 PR 18-NOV-1998; 98US-0108858.
 PR 18-NOV-1998; 98US-0108904.

XX (GETH) GENENTECH INC.

XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

XX WPI; 2000-237871/20.

XX P-PSDB; AAY99450.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
 Claim 2; Fig 22L; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.

XX SQ Sequence 497 BP; 201 A; 95 C; 104 G; 95 T; 2 other;

Query Match 18.9%; Score 95.6; DB 21; Length 497;
 Best Local Similarity 63.5%; Pred. No. 8.8e-15;

Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 40 GTTCTGTCACAGCTCAGCGAGCCTGCTCAACCTGAAGGCCATGCTGGAGCGGTCACA 99
 Db 68 GGTGTGATTCCATCCAGGGGGGATCCTCAACCTGAACCAAGATGTCGAAGCAATGACT 127
 Qy 100 GGGAGGAGCGCCATCCTCTCTTCTGGGGGTACGGTTGCTACTGTGGTGGGGGGCGGT 159
 Db 128 GGGAAATGCCCACCTCTCTCTACTGCGCCCTACGGGTGCTCACTCGCGACTAGTGGCACA 187
 Qy 160 GGCAGGCCCAAGGATGAGTGGTGGTGTGCTGCCAGCCCGCAGCTGCTGCTACCAAGGA 219
 Db 188 GGCACACCAAGATGCCAGGACTGGTGTGCTGCCACCCATGATGCTGCTATGACCCAC 247
 Qy 220 CTCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACCAT 269
 Db 248 CTGAAGACCCAGGGGTGCGGCATCTACAAGGACAAACAACAAAGCAGCAT 297

RESULT 12

AAQ81136

ID AAQ81136 standard; cDNA; 4325 BP.

XX AAQ81136;

XX AC

XX DT

XX 15-AUG-1995 (first entry)

XX DE

XX RPLA2-8 gene.

XX

us-09-975-456b-1.rng

Mon Feb 10 11:35:46 2003

XX KW RPLA2-8; phospholipase A2; PLA2; Batten disease; neuronal ceroid lipofuscinosis; gene therapy; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 722..1198

XX FT /*tag= a

XX PN W09502328-A.

XX PD 26-JAN-1995.

XX PF 15-JUL-1994; 94WO-US07926.

XX PR 15-JUL-1993; 93US-0091941.

XX PR 26-JUL-1993; 93US-0097354.

XX PA (INCY-) INCYTE PHARM INC.

XX PA (INDV) UNIV INDIANA FOUND.

XX PI Seilhamer JJ, Tischfield JA;

XX DR WPI; 1995-067096/09.

XX DR P-PSDB; AAR63044.

XX PT Novel type III and IV low mol. wt. phospholipase A2 enzymes -

XX PT from humans and rats, also nucleic acid sequences useful, e.g.

XX PT for recombinant prodn. of enzymes, research into Batten's

XX PT disease, etc.

XX PS Disclosure; Page 57-60; 160pp; English.

XX CC A human PLA2-encoding cDNA (AAQ81137) expressing HPLA2-10, was

XX CC isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,

XX CC designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated

XX CC from rat brain and heart cDNA libraries, respectively. A partial human

XX CC genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.

XX CC RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10

XX CC and HPLA2-10 as type IV.

XX SQ Sequence 4325 BP; 1046 A; 1086 C; 1242 G; 951 T; 0 other;

Query Match 17.0%; Score 86.4; DB 16; Length 4325;

Best Local Similarity 60.0%; Pred. No. 3.6e-12;

Matches 144; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 47 CCACAGCTCAGCGAGCCTGCTCAACCTGAAGCCATGGTGGAGCGGCTCACAGGGAGGA 106

DB 792 COTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACATCACGGGGCGCA 851

QY 107 GGGCCATCTGTCCTTCTGGCTACGCTTGTCTACTGTGGGCTGGGGCGGTGGCCAGC 166

DB 852 GGGCCCTCTTCTCTTATACGATATGCTGCTACTGTGGGCTGGGGCGAGGATCC 911

QY 167 CCAAGGATCAGTGGAGCTGGTGTGCTGCCACGCCAGCAGTGTGTCTACAGAACTCTTTG 226

DB 912 CTGTGGAGCCACAGACAGGTGCTGCTGGGCTCATGATGTTGTGTACCAAGCTTAAGG 971

QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCATCGAGAACACACTGAGA 286

DB 972 AATATGGCTGGCAGCCCATCTTGAATGCTATCAGTTTGCATTTGTCAACGGGACCGTGA 1031

RESULT 13

AAQ81137

ID AAQ81137 standard; cDNA; 1828 BP.

XX AAQ81137;

XX AC

XX DT 15-AUG-1995 (first entry)

XX XX

XX DE RPLA2-10 gene.

XX KW RPLA2-10; phospholipase A2; PLA2; Batten disease; neuronal ceroid lipofuscinosis; gene therapy; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 233..646

XX FT /*tag= a

XX PN W09502328-A.

XX PD 26-JAN-1995.

XX PF 15-JUL-1994; 94WO-US07926.

XX PR 15-JUL-1993; 93US-0091941.

XX PR 26-JUL-1993; 93US-0097354.

XX PA (INCY-) INCYTE PHARM INC.

XX PA (INDV) UNIV INDIANA FOUND.

XX PI Seilhamer JJ, Tischfield JA;

XX DR WPI; 1995-067096/09.

XX DR P-PSDB; AAR63045.

XX PT Novel type III and IV low mol. wt. phospholipase A2 enzymes -

XX PT from humans and rats, also nucleic acid sequences useful, e.g.

XX PT for recombinant prodn. of enzymes, research into Batten's

XX PT disease, etc.

XX PS Disclosure; Page 63-64; 160pp; English.

XX CC A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was

XX CC isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,

XX CC designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated

XX CC from rat brain and heart cDNA libraries, respectively. A partial human

XX CC genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.

XX CC RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10

XX CC and HPLA2-10 as type IV.

XX SQ Sequence 1828 BP; 426 A; 485 C; 489 G; 428 T; 0 other;

Query Match 16.3%; Score 82.8; DB 16; Length 1828;

Best Local Similarity 56.7%; Pred. No. 2.3e-11;

Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1 ATCAAGAAGTTCTTCCCGTGGCCATCCTTGTGTCGACGCGTTCGTCTCCACAGCTCACGGC 60

DB 233 ATGAAGCGCTCTCTCAGCTGGCTTGTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 292

QY 61 AGCCTGCTCAACCTGAAGCCATGTGGAGCGGTACAGGGAGGAGCGCCATCTCTGTCC 120

DB 293 GGCTTGTCTAGAACTGAAGTCCATGATGAGAGGTGACTGGGAAGTATCCGCTTAAGAAC 352

QY 121 TTGCTGGGCTACGCTTGTCTACTGTGGCTGGGGGCGGTGGCCAGCCAGAGATGAGGTG 180

DB 353 TATGGCTTCTACGGCTGCTACTGTGCTGGGCGGCCACGGACCCCTTAAGGATGCACT 412

QY 181 GACTGTGCTGCCACGCCACGACTGCTGTGTACAGAACTCTTTGACCAAGGCTGTAC 240

DB 413 GATTGTGCTGTCGGATGTCAGACCGCTTGTATGGGCTACTGGAGGAGAAACACTGTGCC 472

QY 241 CCCTATGTGGACCACTATGATCACACCATC 270

DB 473 ATCCGGACCCAGTCCCTATGACTACAGATTC 502

RESULT 14

AAQ72076

ID AAQ72076 standard; cDNA; 1233 BP.

XX

us-09-975-456b-1.rng

Mon Feb 10 11:35:46 2003

XX KW RPLA2-8; phospholipase A2; PLA2; Batten disease; neuronal ceroid lipofuscinosis; gene therapy; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 722..1198

XX FT /*tag= a

XX PN W09502328-A.

XX PD 26-JAN-1995.

XX PF 15-JUL-1994; 94WO-US07926.

XX PR 15-JUL-1993; 93US-0091941.

XX PR 26-JUL-1993; 93US-0097354.

XX PA (INCY-) INCYTE PHARM INC.

XX PA (INDV) UNIV INDIANA FOUND.

XX PI Seilhamer JJ, Tischfield JA;

XX DR WPI; 1995-067096/09.

XX DR P-PSDB; AAR63044.

XX PT Novel type III and IV low mol. wt. phospholipase A2 enzymes -

XX PT from humans and rats, also nucleic acid sequences useful, e.g.

XX PT for recombinant prodn. of enzymes, research into Batten's

XX PT disease, etc.

XX PS Disclosure; Page 57-60; 160pp; English.

XX CC A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was

XX CC isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,

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XX CC from rat brain and heart cDNA libraries, respectively. A partial human

XX CC genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.

XX CC RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10

XX CC and HPLA2-10 as type IV.

XX SQ Sequence 4325 BP; 1046 A; 1086 C; 1242 G; 951 T; 0 other;

Query Match 17.0%; Score 86.4; DB 16; Length 4325;

Best Local Similarity 60.0%; Pred. No. 3.6e-12;

Matches 144; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 47 CCACAGCTCAGCGAGCCTGCTCAACCTGAAGCCATGGTGGAGCGGCTCACAGGGAGGA 106

DB 792 COTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACATCACGGGGCGCA 851

QY 107 GGGCCATCTGTCCTTCTGGCTACGCTTGTCTACTGTGGGCTGGGGCGGTGGCCAGC 166

DB 852 GGGCCCTCTTCTCTTATACGATATGCTGCTACTGTGGGCTGGGGCGAGGATCC 911

QY 167 CCAAGGATCAGTGGAGCTGGTGTGCTGCCACGCCAGCAGTGTGTCTACAGAACTCTTTG 226

DB 912 CTGTGGAGCCACAGACAGGTGCTGCTGGGCTCATGATGTTGTGTACCAAGCTTAAGG 971

QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACACCATCGAGAACACACTGAGA 286

DB 972 AATATGGCTGGCAGCCCATCTTGAATGCTATCAGTTTGCATTTGTCAACGGGACCGTGA 1031

RESULT 13

AAQ81137

ID AAQ81137 standard; cDNA; 1828 BP.

XX AAQ81137;

XX AC

XX DT 15-AUG-1995 (first entry)

XX XX

XX DE RPLA2-10 gene.

XX KW RPLA2-10; phospholipase A2; PLA2; Batten disease; neuronal ceroid lipofuscinosis; gene therapy; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 233..646

XX FT /*tag= a

XX PN W09502328-A.

XX PD 26-JAN-1995.

XX PF 15-JUL-1994; 94WO-US07926.

XX PR 15-JUL-1993; 93US-0091941.

XX PR 26-JUL-1993; 93US-0097354.

XX PA (INCY-) INCYTE PHARM INC.

XX PA (INDV) UNIV INDIANA FOUND.

XX PI Seilhamer JJ, Tischfield JA;

XX DR WPI; 1995-067096/09.

XX DR P-PSDB; AAR63045.

XX PT Novel type III and IV low mol. wt. phospholipase A2 enzymes -

XX PT from humans and rats, also nucleic acid sequences useful, e.g.

XX PT for recombinant prodn. of enzymes, research into Batten's

XX PT disease, etc.

XX PS Disclosure; Page 63-64; 160pp; English.

XX CC A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was

XX CC isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,

XX CC designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated

XX CC from rat brain and heart cDNA libraries, respectively. A partial human

XX CC genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.

XX CC RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10

XX CC and HPLA2-10 as type IV.

XX SQ Sequence 1828 BP; 426 A; 485 C; 489 G; 428 T; 0 other;

Query Match 16.3%; Score 82.8; DB 16; Length 1828;

Best Local Similarity 56.7%; Pred. No. 2.3e-11;

Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1 ATCAAGAAGTTCTTCCCGTGGCCATCCTTGTGTCGACGCGTTCGTCTCCACAGCTCACGGC 60

DB 233 ATGAAGCGCTCTCTCAGCTGGCTTGTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 292

QY 61 AGCCTGCTCAACCTGAAGCCATGTGGAGCGGTACAGGGAGGAGCGCCATCTCTGTCC 120

DB 293 GGCTTGTCTAGAACTGAAGTCCATGATGAGAGGTGACTGGGAAGTATCCGCTTAAGAAC 352

QY 121 TTGCTGGGCTACGCTTGTCTACTGTGGCTGGGGGCGGTGGCCAGCCAGAGATGAGGTG 180

DB 353 TATGGCTTCTACGGCTGCTACTGTGCTGGGCGGCCACGGACCCCTTAAGGATGCACT 412

QY 181 GACTGTGCTGCCACGCCACGACTGCTGTGTACAGAACTCTTTGACCAAGGCTGTAC 240

DB 413 GATTGTGCTGTCGGATGTCAGACCGCTTGTATGGGCTACTGGAGGAGAAACACTGTGCC 472

QY 241 CCCTATGTGGACCACTATGATCACACCATC 270

DB 473 ATCCGGACCCAGTCCCTATGACTACAGATTC 502

RESULT 14

AAQ72076

ID AAQ72076 standard; cDNA; 1233 BP.

XX

us-09-975-456b-1.rng

Mon Feb 10 11:35:46 2003

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QY 39 CGTTCTGTCCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCAC 98
Db 71 CGGTATAACTGCNAACCCAGGAGGGCTCCTGAACCTGAACAAGATGGTACACACATGAC 130
QY 99 AGGGAGAGCGGCCATCCTGTCTTGTGGCTACGGTTGCTACTGTGGGCTGGGGGGCG 158
Db 131 GGGGAAGAAAGCCTTCTCAGCTACTTGGCCCTACGGCTGTCTACTGTGGACTGGTGGCA 190
QY 159 TGGCCAGCCCAAGGATGAGGTGACTGGTGTGCTGCCACGCCACGACTGCTGTACCA 218
Db 191 AGGGCAACCCAAAGATGCCACAGACTGGTGTGCTCAGAAGCATGATTGTTGATGCCCA 250
QY 219 ACTCTTTTGACCAAGGCTGTCCACCCCTTATGTGGACCCTATGATCACCACCATCGA 278
Db 251 CCTGAGATCGATGGATGCAAGAGCCTGACAGACAACCTACAATACAGCATCTCCAG 310
QY 279 CACTGAGATAGTCTGCAGTGACCTCAACAAGACAGAGTGTGACAAGCAGACATGCA 338
Db 311 CACT-----ATCCAGTCTCTGACAACGGGGAGCTGGTGTGAAAGGCAACTGTGCT 364
QY 339 TGACAAGAATGGTCTGTGCTGTATGAACACAGAGTACCGAGAGGAGTACCG 392
Db 365 TGACAAGGAGTGGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGCG 418

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Search completed: February 8, 2003, 04:30:03
Job time : 232 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:30:09 ; Search time 47 Seconds
(without alignments)
3308.194 Million cell updates/sec

Title: US-09-975-456B-1
Perfect score: 507
Sequence: 1 atgaagaagttcttcacgt.....cgcccccgccctccctag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	88	17.4	4325	2	US-08-888-497-21		Sequence 21, Appl
2	88	17.4	4325	4	US-09-362-230-21		Sequence 21, Appl
3	88	17.4	4325	5	PCT-US94-07926-21		Sequence 21, Appl
4	82.8	16.3	1828	2	US-08-888-497-29		Sequence 29, Appl
5	82.8	16.3	1828	4	US-09-362-230-29		Sequence 29, Appl
6	82.8	16.3	1828	5	PCT-US94-07926-29		Sequence 29, Appl
7	76.8	15.1	1014	2	US-08-888-497-31		Sequence 31, Appl
8	76.8	15.1	1014	4	US-09-362-230-31		Sequence 31, Appl
9	76.8	15.1	1014	5	PCT-US94-07926-31		Sequence 31, Appl
10	75.8	15.0	742	3	US-08-966-317-2		Sequence 2, Appl
11	75.8	15.0	742	4	US-09-489-770-2		Sequence 2, Appl
12	57.8	11.4	479	1	US-08-186-895-9		Sequence 9, Appl
13	54	10.7	151	2	US-08-888-497-26		Sequence 26, Appl
14	54	10.7	151	4	US-09-362-230-26		Sequence 26, Appl
15	54	10.7	151	5	PCT-US94-07926-26		Sequence 26, Appl
16	48.2	9.5	15328	2	US-08-888-497-33		Sequence 33, Appl
17	48.2	9.5	15328	4	US-09-362-230-33		Sequence 33, Appl
18	48.2	9.5	15328	5	PCT-US94-07926-33		Sequence 33, Appl
19	47.6	9.4	151	2	US-08-888-497-25		Sequence 25, Appl
20	47.6	9.4	151	4	US-09-362-230-25		Sequence 25, Appl
21	47.6	9.4	151	5	PCT-US94-07926-25		Sequence 25, Appl
22	40.8	8.0	5163	3	US-08-700-651-1		Sequence 1, Appl
23	40.8	8.0	5163	3	US-08-928-361B-4		Sequence 4, Appl
24	40.8	8.0	5318	3	US-08-700-651-2		Sequence 2, Appl
25	40.8	8.0	5318	3	US-08-928-361B-3		Sequence 3, Appl
26	36.8	7.3	536	4	US-09-465-558-33		Sequence 33, Appl
27	36.6	7.2	1288	1	US-08-440-856A-9		Sequence 9, Appl

28	36.6	7.2	5511	3	US-08-928-361B-2	Sequence 2, Appl
29	36.6	7.2	7334	3	US-08-928-361B-1	Sequence 1, Appl
30	36.2	7.1	1187	1	US-08-440-856A-2	Sequence 2, Appl
31	35.6	7.0	3468	1	US-07-951-715A-2	Sequence 2, Appl
32	35.6	7.0	3468	2	US-08-459-448A-2	Sequence 2, Appl
33	35.6	7.0	3468	3	US-08-459-595A-2	Sequence 2, Appl
34	35.6	7.0	3468	3	US-08-459-504B-2	Sequence 2, Appl
35	35.6	7.0	3468	3	US-08-459-444-2	Sequence 2, Appl
36	35.6	7.0	3468	3	US-09-053-549-3	Sequence 3, Appl
37	35.6	7.0	3468	4	US-09-547-422-2	Sequence 2, Appl
38	35.6	7.0	4523	4	US-09-473-716-1	Sequence 3, Appl
39	35.2	6.9	360	4	US-09-060-756-455	Sequence 1, Appl
40	35.2	6.9	1920	4	US-09-160-496-4	Sequence 455, App
41	35	6.9	1806	2	US-08-980-060-1	Sequence 4, Appl
42	35	6.9	1806	4	US-09-307-185-1	Sequence 1, Appl
43	35	6.9	3459	2	US-08-980-060-3	Sequence 3, Appl
44	35	6.9	3459	4	US-09-307-185-3	Sequence 3, Appl
45	34.4	6.8	13842	4	US-09-105-537-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-888-497-21
; Sequence 21, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

NAME/KEY: CDS
LOCATION: 722..1195
US-09-362-230-21

Query Match 17.4%; Score 88; DB 4; Length 4325;
Best Local Similarity 60.4%; Pred. No. 2e-14;
Matches 145; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 47 CCACAGCTCAGCGCAGCTGCTCAACCTGAAGGCCATGTTGGAGGCCGTCAACAGGAGGA 106
DB 792 CCTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACACATCACGGGGCGCA 851
QY 107 GCGCCATCTGCTCTCTGCTGGGCTACGGTGTCTACTGTGGGCTGGGGGGCGGCGCCAGC 166
DB 852 GCGCTTCTCTCTCTATACGATATGGCTGCTACTGTGGGCTTGGGGCGGAGGATCC 911
QY 167 CAAGGATGAGTGAGTGGTGTGCTGCCAGCCACGACTGCTGTACACAGGAACCTTTTG 226
DB 912 CTGTGGAGCCACAGACAGTGTCTGTGGGCTCATGACTGTTGCTACCAACAAGCTTAAGG 971
QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACATCGAGACACACTGAGA 286
DB 972 AATATGCTGCCAGCCATCTTGAATGCTATCATAGTTTGCATTTGTCAACGGGACCGTGA 1031

RESULT 3
PCT-US94-07926-21
Sequence 21, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 722..1195

NAME/KEY: CDS
LOCATION: 722..1195
US-08-888-497-21

Query Match 17.4%; Score 88; DB 2; Length 4325;
Best Local Similarity 60.4%; Pred. No. 2e-14;
Matches 145; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 47 CCACAGCTCAGCGCAGCTGCTCAACCTGAAGGCCATGTTGGAGGCCGTCAACAGGAGGA 106
DB 792 CCTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACACATCACGGGGCGCA 851
QY 107 GCGCCATCTGCTCTCTGCTGGGCTACGGTGTCTACTGTGGGCTGGGGGGCGGCGCCAGC 166
DB 852 GCGCTTCTCTCTCTATACGATATGGCTGCTACTGTGGGCTTGGGGCGGAGGATCC 911
QY 167 CAAGGATGAGTGAGTGGTGTGCTGCCAGCCACGACTGCTGTACACAGGAACCTTTTG 226
DB 912 CTGTGGAGCCACAGACAGTGTCTGTGGGCTCATGACTGTTGCTACCAACAAGCTTAAGG 971
QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACATCGAGACACACTGAGA 286
DB 972 AATATGCTGCCAGCCATCTTGAATGCTATCATAGTTTGCATTTGTCAACGGGACCGTGA 1031

RESULT 2
US-09-362-230-21
Sequence 21, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:

PCT-US94-07926-21

Query Match	17.4%	Score 88;	DB 5;	Length 4325;
Best Local Similarity	60.4%	Prod. No. 2e-14;		
Matches 145;	Conservative 0;	Mismatches 95;	Indels 0;	Gaps 0;
QY	47	CCACAGCTCAGCGCAGCCTGCTCAACTGAAGCCCATGGTGGAGCCGTCACAGGAGGA	106	
Db	792	CTCCACCCCTCAGCAGCTTCTGGCAGTTCAGAGGATGGTCAACACATCAGCGGGCGCA	851	
QY	107	GGCCATCCTTCCTTCTGGGCTACGGTTGCTACTGTGGGCTGGGGGCCGTGGCCAGC	166	
Db	852	GGCCCTTCTTCCTATTACGGATATGGCTGCTACTGTGGCTTGGGGCCAGGGATCC	911	
QY	167	CAAGGATGAGGTGGACTGGTGTGCCACGCCACACACTGCTGCTACCAAGGAACTCTTG	226	
Db	912	CTGTGGAGCCACAGACAGGTGCTGTGGGCTCATGACTGTGCTACCAACAGCTTAAAG	971	
QY	227	ACCAAGGCTGTACCCCTATGTGGACCACATATGATCACACCATCGAGAACAACTGAGA	286	
Db	972	ATATGGCTGCCACCCCATCTTGAATGCCCTATCAGTTTGCCATTGTCAACGGGACCGTGA	1031	

RESULT 4

US-08-888-497-29
: Sequence 29, Application US/08888497
: Patent No. 5972677
: GENERAL INFORMATION:
: APPLICANT: Tischfield, Jay A.
: TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
: TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
: TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
: TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
: ADDRESSEE: Russell PA
: STREET: 200 East Broward Boulevard
: CITY: Fort Lauderdale
: STATE: FL
: COUNTRY: USA
: ZIP: 33301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/888,497
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/651,405
: FILING DATE:
: APPLICATION NUMBER: US 08/097,354
: FILING DATE: 26-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Manso, Peter J.
: REGISTRATION NUMBER: 32,264
: REFERENCE/DOCKET NUMBER: IN21044-5
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 305-527-2498
: TELEFAX: 305-764-4996
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1828 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS

RESULT 5

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US-09-362-230-29
: Sequence 29, Application US/09362230
: Patent No. 6352849
: GENERAL INFORMATION:
: APPLICANT: Tischfield, Jay A.
: APPLICANT: Seilhamer, Jeffrey J.
: TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
: TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
: TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
: TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
: ADDRESSEE: Russell PA
: STREET: 200 East Broward Boulevard
: CITY: Fort Lauderdale
: STATE: FL
: COUNTRY: USA
: ZIP: 33301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/09/362,230
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: PRIOR APPLICATION NUMBER: 08/888,497
: FILING DATE:
: APPLICATION NUMBER: US 08/097,354
: FILING DATE: 26-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Manso, Peter J.
: REGISTRATION NUMBER: 32,264
: REFERENCE/DOCKET NUMBER: IN21044-5
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 305-527-2498
: TELEFAX: 305-764-4996
: INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1828 base pairs
: TYPE: nucleic acid

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: LOCATION: 233..643
US-08-888-497-29

Query Match      16.3%:   Score 82.8:   DB 2:   Length 1028;
Best Local Similarity 56.7%:   Pred No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY      1  ATGAAGAAGTCTTCACCGTGGCCCATCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC 60
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Db      233  ATGAAGCGCCCTCCACGCGTGGCTTGTCTTGCAGTGTGCTGCAGTCCCAAGG 292
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QY      61  AGCCTGCTCAACCTGAAGGCCATGTGGAGGCCGTACACGGAGGAGCGCCATCTGTGTC 120
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Db      293  GGCCTTGCTAGAACTGAAGTCCATGATTTGAAGAAGTGACTGGGAAGAATGCCGTTAAAGAAC 352
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QY      121  TTCTGGGGCTACGGTTGCTACTGTGGGCTGGGGGGCGGTGGCCAGGCCCAAGGATGAGGTG 180
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Db      353  TATGGCTTCTACGGCTGCTACTGTGGCTGGGGGGCGCCACGGGACCCTTAAGGATGGCACT 412
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY      181  GACTGTGCTGCCAGGCCACGACTGCTGCTACCAAGAACTCTTTGACCAGGCTGTGCAC 240
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      413  GATTGGTGCTGTCCGATGCACGACCGTTGTTATGGGCTACTGGAGGAGAAACACTGTGCC 472
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY      241  CCTATGTGGACCACATGATGATCAACCATC 270
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      473  ATCCGAGCCAGCTCCCTGACTACAGATTC 502
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 233..643
; /s-09-362-230-29

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Query Match 16.3%; Score 82.8; DB 4; Length 1828;
Best Local Similarity 56.7%; Pred. No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY	1	ATGAGAGAGTTCTTACCGTGGCCATCTTGTCGCAGCGTTCTGTCCACAGCTCAAGGC	60
Db	233	ATGAGAGCGCTCTCAGCTGGCTTGTCTCTGGCTTGCAGTGTCCGTGCACTCCAGG	292
QY	61	AGCCTGCTCAACTGAAGCCCATGTTGGAGGCCGTCACAGGAGGAGCGCCATCTGTGCC	120
Db	293	GGCTTGCTAGAACTGAAGTGCATGATTGAGAGGTCAGCTGGGAGCAATCCGCTAAGAAC	352
QY	121	TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCCGTGGCCAGCCCAAGATCAGGTG	180
Db	353	TATGGGCTTCTACGGCTGCTACTGTGCTGGGGGCCCGCCAGGCCCTAAGGATGGCACT	412
QY	181	GACTGTGTGTCGCCACGCCACGACTGCTGTACCGAGAACTCTTTGACCACGGCTGCAC	240
Db	413	GATTGGTGTCTCGGATGACGACCGCTGTTATGGGCTACTGGAGGAGAAACACTGTGCC	472
QY	241	CCCTATGTGGACCACTATGATCACGCATC	270
Db	473	ATGCGGACCCCTCTTCTTACTACTACGATTC	502

RESULT 6

PCT-US94-07926-29
Sequence 29, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 1828 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 233..643
; /CDT=HIS94-079266-29

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Query Match 16.3%; Score 82.8; DB 5; Length 1828;
Best Local Similarity 56.7%; Pred. No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0

QY	1	ATCAAGAAGTCTCTTCAACCGTGGCCATCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC	60
Db	233	ATGAGGCGCTCTCACTACGCTGGTTCCTGGTGTGCAGTGTGCTGCGATCCATCCAGGG	292
QY	61	AGCCTGCTCAACCTGAAGCGCCATGTGGAGGCGCTCACAGGAGGAGAGCGCCATCTCTGTCC	120
Db	293	GGCTTGTGAACTGAAGTCCATGATTTGAGAAGGTGACTTGGGAAGAATGCCCTGAAGAAC	352
QY	121	TTCTGGGGCTACCGTTGCTACTGTGGCTGGGGGCGCTGGCCAGCCCAAGATGAGGTG	180
Db	353	TATGGCTCTTACGGCTGCTACTGTGGCTGGGGCGCCACGGGACCCCTAAGGATGGCACT	412
QY	181	GACTGGTGCTGCCACGCCACGACTGCTGTACCGAAGACTTTTGCACCAAGGCTGTCAAC	240
Db	413	GATTGGTGCCTGCGGATGTCACGCCCTGTGTATGGGGCTACTGGAGGAGAAACACTGTGCC	472
QY	241	CCCTATGTGGACCACTATGATCACACCATC	270
Db	473	ATCCGGGACCCAGTCTCTATGACTACAGATTG	502

DECLASSIFIED 7

RE5041
 US-08-888-497-31
 ; Sequence 31, Application US/08888497
 ; Patent No. 5972677
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Tischfield, Jay A.
 ;
 ; APPLICANT: Seilhamer, Jeffrey J.
 ;
 ; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
 ;
 ; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
 ;
 ; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
 ;
 ; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
 ;
 ; NUMBER OF SEQUENCES: 44
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ;
 ; ADDRESSEE: Russell PA
 ;
 ; STREET: 200 East Broward Boulevard
 ;
 ; CITY: Fort Lauderdale
 ;
 ; STATE: FL
 ;
 ; COUNTRY: USA
 ;
 ; ZIP: 33301
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: Floppy disk
 ;
 ; COMPUTER: IBM PC compatible
 ;
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/888,497
 ;
 ; FILING DATE:
 ;
 ; CLASSIFICATION:
 ;
 ; PRIOR APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/651,405
 ;
 ; FILING DATE:
 ;
 ; APPLICATION NUMBER: US 08/097,354
 ;
 ; FILING DATE: 26-JUL-1993
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Manso, Peter J.
 ;
 ; REGISTRATION NUMBER: 32,264
 ;
 ; REFERENCE/DOCKET NUMBER: IN21044-5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2498
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1014 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 131..544
 US-08-888-497-31

Query Match 15.1%; Score 76.8; DB 2; Length 1014;
 Best Local Similarity 57.5%; Pred. No. 1.2e-11;
 Matches 138; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCCTGCTCCACAGCTCAGCGC 60
 Db 131 ATGAAGAGCCCTCTCCCACTGGCTTGTGCTTGTAGTGTGCTGCTGTGCAAGGA 190

Qy 61 AGCTGTCTCAACCTGAAGCCATGGTGGAGGCGCTCACAGGAGGAGGCCCATCTCTGTCC 120
 Db 191 GGCTTGTGGACCTTAAATCAATGATCGAGAAGGTGACAGGGAAGAACGCCCTGACAAAC 250

Qy 121 TTCCTGGGCTACGGTGTCTACTGTGGCTGGGGGGCGGTGGCCAGCCCAAGGATGAGGTG 180
 Db 251 TACGGCTTCTACGGCTGTACTCGGCTGGGGGGCGGAGGAAACCCCAAGGATGGCAC 310

Qy 181 GACTGTGTCTGCGCCACGCCACGACTGCTGTACAGGAACCTCTTTGACCAAGGCTGTGCAC 240
 Db 311 GATTGGTGTCTTGGCGCATGACCACTGCTATGGCGGCTGGAGGAGGAGGCTGCAAC 370

RESULT 8
 US-09-362-230-31
 Sequence 31, Application US/09362230
 Patent No. 6352849
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 APPLICANT: Seilhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
 TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
 TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESS: Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/09/362,230
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/888,497
 FILING DATE:
 APPLICATION NUMBER: US 08/097,354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2498
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1014 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 131..544
 US-09-362-230-31

Query Match 15.1%; Score 76.8; DB 4; Length 1014;
 Best Local Similarity 57.5%; Pred. No. 1.2e-11;
 Matches 138; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTTCCTGCTCCACAGCTCAGCGC 60
 Db 131 ATGAAGAGCCCTCTCCCACTGGCTTGTGCTTGTAGTGTGCTGCTGTGCAAGGA 190

Qy 61 AGCTGTCTCAACCTGAAGCCATGGTGGAGGCGCTCACAGGAGGAGGCCCATCTCTGTCC 120
 Db 191 GGCTTGTGGACCTTAAATCAATGATCGAGAAGGTGACAGGGAAGAACGCCCTGACAAAC 250

Qy 121 TTCCTGGGCTACGGTGTCTACTGTGGCTGGGGGGCGGTGGCCAGCCCAAGGATGAGGTG 180
 Db 251 TACGGCTTCTACGGCTGTACTCGGCTGGGGGGCGGAGGAAACCCCAAGGATGGCAC 310

Qy 181 GACTGTGTCTGCGCCACGCCACGACTGCTGTACAGGAACCTCTTTGACCAAGGCTGTGCAC 240
 Db 311 GATTGGTGTCTTGGCGCATGACCACTGCTATGGCGGCTGGAGGAGGAGGCTGCAAC 370

RESULT 9
 PCT-US94-07926-31
 Sequence 31, Application PC/TUS9407926
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 APPLICANT: Seilhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
 TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
 TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESS: Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: PCT/US94/07926
 FILING DATE: 15-JUL-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/097,354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:

Mon Feb 10 11:35:47 2003

TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVAUTUT01
CLONE: 816403
US-08-966-317-2

Query Match 15.1%; Score 76.8; DB 5; Length 1014;
Best Local Similarity 57.5%; Pred. No. 1.2e-11;
Matches 138; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTCCACGTGGCCATCCTTCTGCGACGCTTCTGTCCACAGCTCAGGC 60
Db 131 ATGAAGGCTCTCTCCACTGGCTTGGTTCTCTGGCTTGTAGTGGCTGTGCTGCAAGGA 190
QY 61 AGCTTGCTCAACTGAAGCCATGTGGAGCGCGTCACAGGAGGAGCGCCATCCTGTCC 120
Db 191 GGCTTGCTGGACCTAAATCAATGATCGAAGGTGACAGGGAAGAGCGCCCTGACAAAC 250
QY 121 TTCTGGGCTACGTTGCTTACTGTGGGTGGGGGCGCTGGCCAGCCCAAGGATGAGGTG 180
Db 251 TACGGCTTCTACGGCTTACTGCGGCTGGGGCGCGGAGGAACCCCAAGGATGGGACC 310
QY 181 GACTGTGTGCCACCCACCACTGCTGCTACAGGAACCTTTTGACCAAGGCTGTAC 240
Db 311 GATTGGTGTGTTGGCGCATGACCACTGCTATGGGCGCTGGAGGAGGAGGCTGCAAC 370

RESULT 10
US-08-966-317-2
Sequence 2, Application US/08966317
Patent No. 6103469
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVAUTUT01
CLONE: 816403
US-08-966-317-2

Query Match 15.0%; Score 75.8; DB 3; Length 742;
Best Local Similarity 54.5%; Pred. No. 2.1e-11;
Matches 177; Conservative 0; Mismatches 142; Indels 6; Gaps 1;
QY 110 CCATCTCTCTCTGGCTTACGGTTGCTTACTGTGGGCTGGGGGCGCTGGCCAGCCCA 169
Db 197 CCCCATCGCCTATATGAATATGTTGCTTTTGTGGAGGCGCATGGCCAGCCCC 256
QY 170 AGGATGAGGTGGAGTGTGCTGCCACGCCAGGACTGCTGTACCCAGGAACCTCTTTGACC 229
Db 257 GCGATGCCATTGACTGTGCTGCCATGGCCACGACTGTTGTTACCTCGAGCTGAGGAGG 316
QY 230 AAGGCTGTACCCCTTATCTGGACCATATGATCACACCATCGAGAACAACACTGAGATAG 289
Db 317 CCGGCTGACGCCCCCAAGACAGAGCGCT-----ACTCCTGGCAGTGGCTCAATCAGAGCG 370
QY 290 TCTGCAGTGCACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGTACACAAGAAC 349
Db 371 TCTGTGCGGACCGGACAGAGAAATGCCAAGAACTTTGTGCAAGTGTGACCCAGGAGA 430
QY 350 TGGTTCTGTGCTCATGACAGAGAGTACCGAGAGAGTACCGTGGCTTCTCAATGTCT 409
Db 431 TTGCTAACTGTAGTGGCTTGGCTTAACTGAGTACAACTTAAAGTACCTCTTCTACCCAGTTCC 490
QY 410 ACTGCCAGCGCCCGCCCAACTG 434
Db 491 TATGTGAGCGGACTGCGCCCAAGTG 515

RESULT 11
US-09-489-770-2
Sequence 2, Application US/09489770
Patent No. 6399301
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 742 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT01
; CLONE: 816403
US-09-489-770-2

Query Match 15.0%; Score 75.8; DB 4; Length 742;
Best Local Similarity 54.5%; Pred. No. 2.1e-11;
Matches 177; Conservative 0; Mismatches 142; Indels 6; Gaps 1;
QY 110 CCATCCTGCTCTTGGGGCTAGCGTTGCTACTGTGGGGTGGGGGCCCGTGGCCAGCCCA 169
Db 197 CCCCCATCGCCTATATCAAAATATGTTGCTTTTGTGGCTTGGAGGCCATGGCCAGCCCC 256
QY 170 AGGATGAGGTGGACTGGTGTGCGCCAGCCGACGACTGCTGCTACCAAGAACTCTTTGACC 229
Db 257 GCGATGCCATGACTGGTGTGCGCCAGCAGCTGTTGTTTACACTCGAGCTGAGGAGG 316
QY 230 AAGCGTGTCAACCCCTATGTGGACCACTATGATCACACCACTGACAGAACCACTGAGATAG 289
Db 317 CCGGCTGCGAGCCCAAGACAGAGCGCT-----ACTCCTGGCAGTGGCTCAATCAGCGC 370
QY 290 TCTGCGAGTGCATCAACAGACAGAGTGTGACAGCAGACATGCTGTGTGCAAGTGTGACCAAGAGA 430
Db 371 TCTGTGCGGACGGCGAGAGAACAAATGCAAGAACTGTGTGCAAGTGTGACCAAGAGA 430
QY 350 TGGTTCTGCTGCTATGAACACGAGTACCGAGAGGAGTACCGTGGCTTCTCAATGCTCT 409
Db 431 TTGCTAACTGCTTAGCCCAACTGAGTACAACTTAAAGTACCTCTTCTACCCCCCAGTTCC 490
QY 410 ACTGCCAGGGCCCCAGGCCCAACTG 434
Db 491 TATGTGAGCGCGAGCTCGGCCAAGTG 515

RESULT 12
US-08-186-895-9
; Sequence 9, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosfeld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993

APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 24..455
US-08-186-895-9

Query Match 11.4%; Score 57.8; DB 1; Length 479;
Best Local Similarity 52.2%; Pred. No. 1.2e-06;
Matches 128; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCCTGGCCATCTTGTGTCGAGCGTTCTGTCCACAGCTCCACGSC 60
Db 24 ATGAAGACCTCTCTACTGTTGGCAGTGATCATGATCTTTGGCCTACTGCAGGCCCATGGG 83
QY 61 AGCCTCCTCAACTGAAGGCCATGTTGGAGGCCGTTCACAGGAGGAGGCCCATCTGTGCC 120
Db 84 AATTTGGTGAATTCACAGAATGATCAAGTTGACGACAGGAAAGAACGCCACTCAGT 143
QY 121 TTGCTGGGTAGCGTGTCTACTGTGGGTGGGGGCCGTGGCCAGCCGACCAAGGATGAGTG 180
Db 144 TATGGCTTCTACGGTGGCCACTGTGGCGTGGGTGGCAGAGATCCCCCAAGGATGCAACG 203
QY 181 GACTGGTGTGTCACGCCGCCACGACTGCTGTACAGGAACTCTTTGACCAAGGCTGTGAC 240
Db 204 GATCGCTGCTGTGTCACCTCATGACTGTTGTCTACAAACCTCTGGAGAAACGTTGGATG 263
QY 241 CCCTA 245
Db 264 ACCAA 268

RESULT 13
US-08-888-497-26
; Sequence 26, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESS: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
PCT-US94-07926-26

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Query Match      10.7%   Score 54;   DB 5;   Length 151;
Best Local Similarity 61.3%;   Pred. No. 8.5e-06;
Matches 87;   Conservative 0;   Mismatches 55;   Indels 0;   Gaps 0;

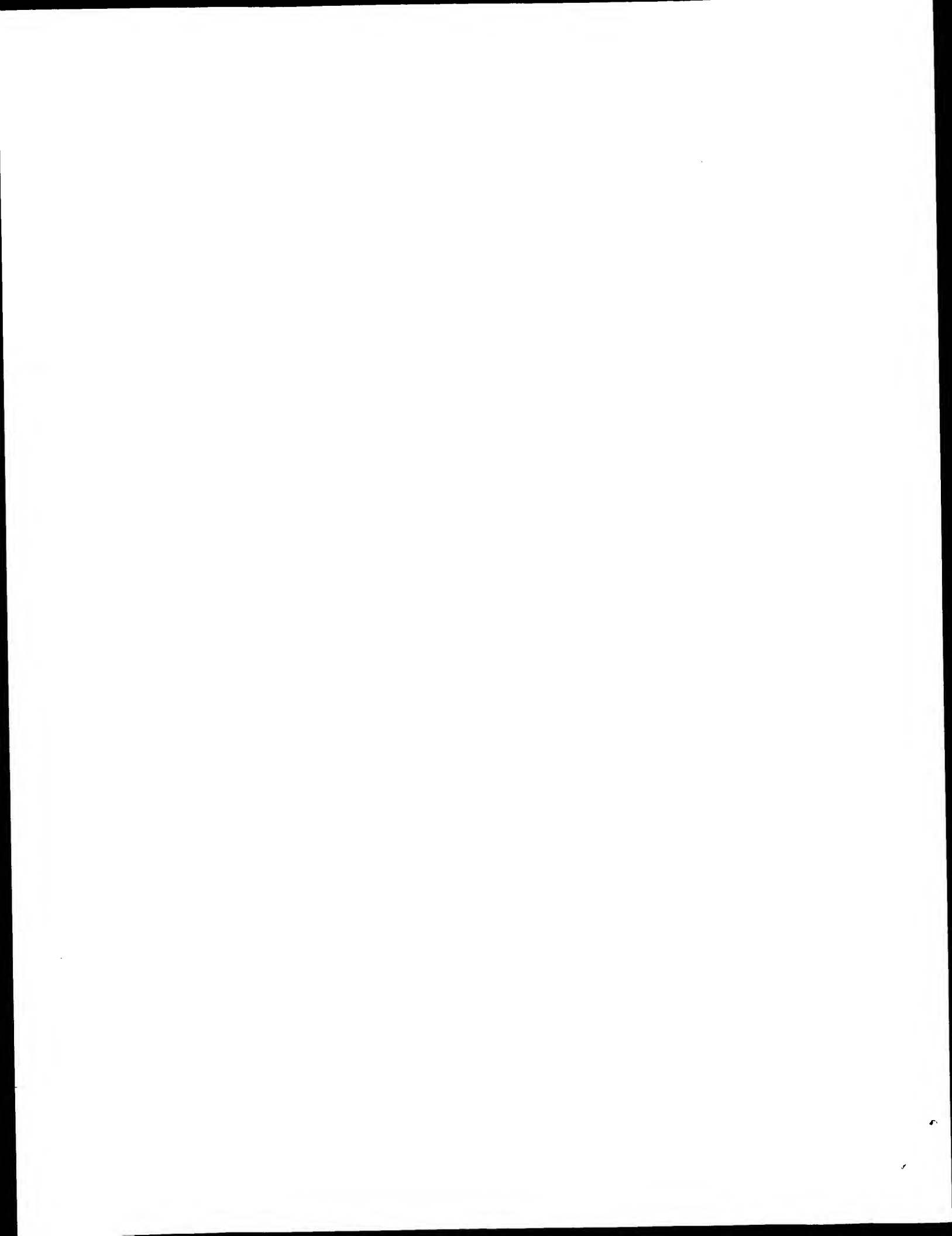
Qy  47 CCACAGCTCAGGAGCGCTGCTCAACCTGAAGGCCATGGTGGAGCGCGTCACAGGGAGGA 106
Db  10 CTTCCACCCCTCAGCAGCTTCTGGCAGTTCCAGAGGATGGTCAACACATCACGGGGCGCA 69

Qy  107 GCGGCATCCTCTCCTTCGTGGGCTACCGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGC 166
Db  70 GCGCCTTCTTCTCTATTACGGATATGGCTGCTACTGTGGCTTGGGGGCCGAGGGATCC 129

Qy  167 CCAAGGATGAGGTGGACTGGTG 188
Db  130 CTGTGGACGCCACAGACAGGTG 151

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Search completed: February 8, 2003, 06:39:31
Job time : 51 secs



us-09-975-456b-1.rnpb

Mon Feb 10 11:35:47 2003

Db 237 CTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT-----TTCC 290
 QY 280 ACTGAGATAGTCTCAGTGCACCTCAACAGACAGAGTGTGACAGCAGACATGTCATGTGT 339
 Db 291 CAGGGGAACATCCACTGCTGTGACAAAGGGAAGCTGTGTGACGACAGCTGTGTGCTGT 350
 QY 340 GACAAGAACATGTTCTGTGCTCATGAACCCAGACGTACCGGAGGAGGTACCG 392
 Db 351 GACAAGGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAAGCG 403

RESULT 3

US-10-028-072-533
 ; Sequence 533, Application US/10028072
 ; Publication No. US20030004311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang
 ; TITLE OF INVENTION:
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/028,072
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059836
 ; PRIOR FILING DATE: 1997-09-24
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062285
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062814
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/062816
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063045
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063082
 ; PRIOR FILING DATE: 1997-10-31

Db 241 CTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT-----TTCC 294
 QY 280 ACTGAGATAGTCTCAGTGCACCTCAACAGACAGAGTGTGACAGCAGACATGTCATGTGT 339
 Db 295 CAGGGGAACATCCACTGCTGTGACAAAGGGAAGCTGTGTGACGACAGCTGTGTGCTGT 354
 QY 340 GACAAGAACATGTTCTGTGCTCATGAACCCAGACGTACCGGAGGAGGTACCG 392
 Db 355 GACAAGGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAAGCG 407

RESULT 2

US-09-835-996A-5
 ; Sequence 5, Application US/09835996A
 ; Patent No. US20020142953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ballinger, Dennis
 ; APPLICANT: Loeb, Debra
 ; APPLICANT: Montgomery, Julie
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhao, Qing
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Drmanac, Radoje
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Qian, Xiahong
 ; APPLICANT: Wang, Durrui
 ; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
 ; FILE REFERENCE: 28110/35915A
 ; CURRENT APPLICATION NUMBER: US/09/835,996A
 ; CURRENT FILING DATE: 2001-04-16
 ; PRIOR APPLICATION NUMBER: US 60/197,137
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: US 09/714,936
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 09/667,298
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: US 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US 09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (18)..(452)
 ; US-09-835-996A-5

Query Match 19.5%; Score 99; DB 10; Length 1931;
 Best Local Similarity 57.2%; Pred. No. 5.8e-18;
 Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCACAGCTCACGGCAGCTGTCTCAACCTGAAGGCCATGTTGGAGCCGTCACA 99
 Db 57 GGTGTGATTCCAATCAGGGCGGATCCTGAACCTGAACAGATGGTCAAGCAAGTGACT 116
 QY 100 GGAAGAGCCGCTCTGCTCTGCTGGCTAGCTGTGCTGGCTGGGGGGCCCGT 159
 Db 117 GGGAAATGCCCATCTCTCTACTGCTCCCTACGGCTGTCACTGGGACTAGTGGCAGA 176
 QY 160 GGCAGCCCAAGGATGAGTGGACTGGTGTGCTGCCAGCCGACGACTGTGCTACAGGAA 219
 Db 177 GGCACCCCAAGATGCTCCAGGACTGGTGTGCTGCCAGCCGACGACTGTGCTATGACCAC 236
 QY 220 CTCTTTGACCAAGGCTGTACCCCTATGTGTGACCACTATGATCACACCATCGAAGAACAC 279

; PRIOR APPLICATION NUMBER: 60/063127
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063327
 ; PRIOR FILING DATE: 1997-10-27
 ; PRIOR APPLICATION NUMBER: 60/063329
 ; PRIOR FILING DATE: 1997-10-27
 ; PRIOR APPLICATION NUMBER: 60/063550
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063561
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063704
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063733
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063735
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063738
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064248
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/064809
 ; PRIOR FILING DATE: 1997-11-07
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065846
 ; PRIOR FILING DATE: 1997-11-17
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/066453
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/069212
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069278
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069334
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069694
 ; PRIOR FILING DATE: 1997-12-16
 ; PRIOR APPLICATION NUMBER: 60/072320
 ; PRIOR FILING DATE: 1998-01-23
 ; PRIOR APPLICATION NUMBER: 60/073612
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: 60/074086
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074092
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079663
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081695
 ; PRIOR FILING DATE: 1998-04-14
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081818

; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082999
 ; PRIOR FILING DATE: 1998-04-24
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085149
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/086414
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/086430
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/088026
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088730
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088741
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088810
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088858
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: 60/089532
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089599
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090538
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 18.98; Score 95.6; DB 9; Length 496;

Best Local Similarity 63.58; Pred. No. 3e-17;

Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCACAGCTACGGCAGCGCTGCTCAACCTGAAGGCCATGGTGGAGCGGTCACA 99

Db 248 CTGAAGACCCAGGGGTGCGGCATCTACAAAGGACAAACAAGAGCAGCAT 297

RESULT 5
US-10-123-904-533
; Sequence 533, Application US/10123904
; Publication No. US20030022328A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1G54

; CURRENT APPLICATION NUMBER: US/10/123,904

; CURRENT FILING DATE: 2002-04-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 396

; OTHER INFORMATION: unknown base

US-10-123-904-533

Query Match 18.9%; Score 95.6; DB 9; Length 496;

Best Local Similarity 63.5%; Pred. No. 3e-17;

Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCCACAGCTCAGCGGAGCCTGCTCAACCTGAAGGCCATGTTGGAGCGCGTCACA 99

Db 68 GGTGTGATTCCCAATCCAGGGGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127

QY 100 GGGAGGAGCGCCATCCTCTCTGCTGGCTACGCTTGTGGCTACGCTTGTGGCTGGGGGGCGGT 159

Db 128 GGGAAATGCCCATCCTCTCTCTACTGGCCCTACGGCTGTCACTGGCGACTAGGTGGCAGA 187

QY 160 GGCCAGCCCAAGGATGAGGTGGAGTGGTGTCTGCCAGCCCGCAGGACTGTGTCTACACAGAA 219

Db 188 GGCCAAACCAAGATGCCACGGAGTGGTGTCTGCCAGACCCATGACTGTGTGTATGACCAC 247

QY 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCATATGATCATCACCAT 269

Db 248 CTGAAGACCCAGGGGTGCGGCATCTACAAAGGACAAACAAGAGCAGCAT 297

RESULT 6

US-10-140-470-533

; Sequence 533, Application US/10140470

; Publication No. US20030022331A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

Db 68 GGTGTGATTCCCAATCCAGGGGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127

QY 100 GGGAGGAGCGCATCCTGTCTCTGCTGGCTACGCTTGTGGCTGGGGGGCGGT 159

Db 128 GGGAAATGCCCATCCTCTCTACTGGCCCTACGGCTGTCACTCGGACTAGGTGGCAGA 187

QY 160 GGCCAGCCCAAGGATGAGGTGGAGTGGTGTGCCACGCCCGCAGGACTGTGTCTACACAGAA 219

Db 188 GGCCAAACCAAGATGCCACGGAGTGGTGTGCCAGACCCATGACTGTGTATGACCAC 247

QY 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCATATGATCATCACCAT 269

Db 248 CTGAAGACCCAGGGGTGCGGCATCTACAAAGGACAAACAAGAGCAGCAT 297

RESULT 4

US-10-121-049-533

; Sequence 533, Application US/10121049

; Publication No. US20030022329A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1G54

; CURRENT APPLICATION NUMBER: US/10/121,049

; CURRENT FILING DATE: 2002-04-12

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 396

; OTHER INFORMATION: unknown base

US-10-121-049-533

Query Match 18.9%; Score 95.6; DB 9; Length 496;

Best Local Similarity 63.5%; Pred. No. 3e-17;

Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCCACAGCTCAGCGGAGCCTGCTCAACCTGAAGGCCATGTTGGAGCGCGTCACA 99

Db 68 GGTGTGATTCCCAATCCAGGGGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127

QY 100 GGGAGGAGCGCCATCCTCTCTGCTGGCTACGCTTGTGGCTGGGGGGCGGT 159

Db 128 GGGAAATGCCCATCCTCTCTACTGGCCCTACGGCTGTCACTCGGACTAGGTGGCAGA 187

QY 160 GGCCAGCCCAAGGATGAGGTGGAGTGGTGTGCCACGCCCGCAGGACTGTGTCTACACAGAA 219

Db 188 GGCCAAACCAAGATGCCACGGAGTGGTGTGCCAGACCCATGACTGTGTATGACCAC 247

QY 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCATATGATCATCACCAT 269

APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P33301C160
 CURRENT APPLICATION NUMBER: US/10/140,470

Prior Filing Date: 2002-05-06
 Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 533

LENGTH: 496

TYPE: DNA

ORGANISM: Homo Sapien

NAME/KEY: unsure

LOCATION: 396

OTHER INFORMATION: unknown base

US-10-140-470-533

Query Match 18.9%; Score 95.6; DB 9; Length 496;
 Best Local Similarity 63.5%; Pred. No. 3e-17;
 Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTGTGCCACAGCTCAGGCGACCTGCTCAACCTGAAGGCCATGGTGAGCGCCGTCA 99
 Db 68 GGTGTGATTCATCCAGGCGGGATCCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127
 QY 100 GCGAGAGGCCCATCTCTGCTGCTGGCTACGGTGTGCTACTGTGGCTGGGGGGCGGT 159
 Db 128 GGGAAATGCCCATCTCTCTCTACTGGCCCTAGCGCTGTCACTGGCGACTAGGTGGCAGA 187
 QY 160 GCGCCGCCAAGGATGAGTGACTGTGCTGCCACGCCACGACTGTGCTATCACCAT 219
 Db 188 GGCACACCAAGATGCCAGGACTGGTGTGCCAGACCCATGACTGTGCTATGACCAC 247
 QY 220 CTCCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCAT 269
 Db 248 CTGAAGACCGGGGTGCGGATCTACAAGGACACACAAAGACGAT 297

RESULT 7

US-10-124-591-2
 Sequence 2, Application US/10124591
 Patent No. US20020177208A1

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.
 Bandman, Olga
 Guegler, Karl J.
 Shah, Purvi
 Corley, Neil C.

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,591

FILING DATE: 16-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/489,770

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/966,317

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0403 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 742 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: OVARTUT01

CLONE: 816403

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-124-591-2

Query Match 15.0%; Score 75.8; DB 9; Length 742;
 Best Local Similarity 54.5%; Pred. No. 1e-11;
 Matches 177; Conservative 0; Mismatches 142; Indels 6; Gaps 1;

QY 110 CCATCTCTGCTCGTGGGTACGGTGTGCTACTGTGGGTGGGGCGGTGCCAGCCCA 169
 Db 197 CCCCCATCGCTATATGAATATGTTGCTTTGTTGGCTTGGGAGCCATGCCAGCCCC 256
 QY 170 AGATCAGGTGGACTGGTCTGCCAGCCCGACGACTGTGCTTACCACTCGAGCTGAGGAGG 316
 Db 257 GCATGCCATGACTGGTGTGCTGCCATGCCAGCTGTTGTTACCTCGAGCTGAGGAGG 289
 QY 230 AAGCTGTCCACCCCTATGTGGACCACTATGATCACCATCGAGAACACACTGAGATAG 370
 Db 317 CCGGTGACGCCGCCAGACAGAGCGCT-----ACTCCTGGCAGTGGCTCAATCAGAGCG 349
 QY 290 TGTGAGTGACCTCAACAAGACAGAGTGTGACAAAGCAGACATGATGTGTGACAAAGA 430
 Db 371 TCTGTGGGACCGGCGCAGAACAAATGCCAAGAACTGTTGTGCAAGTGTGACCCAGGAGA 409
 QY 350 TGGTCTCTGCTCATGAACACGACGTACCGAGAGAGGAGTACCGTGGCTTCTCAATGCT 490
 Db 431 TTGCTAACTGCTTAGCCCCAAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCACTCC 430
 QY 410 ACTGCCAGGCCCCCAGCCCAACTG 434
 Db 491 TATGTGAGCCGCGGACTGCCCAAGTG 515

RESULT 8

US-09-962-832-63/c

Sequence 63, Application US/09962832

Patent No. US2002011082A1

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-74

CURRENT APPLICATION NUMBER: US/09/962,832

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US/60/235,077

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,280

PRIOR FILING DATE: 2000-09-25

NUMBER OF SEQ ID NOS: 259

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or
US-09-962-832-63

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Query Match

Query Match 13.0%; Score 65.8; DB 10; Length 445;
Best Local Similarity 52.6%;
Matches 171; Conservative 0; Mismatches 147; Indels 7; Gaps 1;

	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619
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RESULT 9

US-09-969-708-597 ; Sequence 597, Application US/09969708
; Patent No. US20020102532A1 ; GENERAL INFORMATION:

APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature Sequences

SEQUENCE: 889290-70
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 597
LENGTH: 854
TYPE: DNA
ORGANISM: Homosapiens
S-09-969-708-597

Query Match

Best Local Similarity	11.4%;	Score	57.8;	DB	10;	Length	854;
Matches	128;	Conservative	52.28;	Pred. No.	9.8e-07;	0;	Mismatches
						117;	Indels
						0;	Gaps
						0;	

	QY	DB	QY	1	136	61	Structures	117	Indels	0	Gaps
				ATGAAGAAAGTTCTTCCACGCGTGCCACTCTGTGTGGCAGCGTTCTGTCCACAGCTCAGGC							
				ATGAAGACCCCTCCTACTGTGTGGCAGTATCATGATCTTTGGCCTACTGTGAGGCCCATGG							
				AGCCTGCTCAACTGTGAAGGCCATGGTGGAGGCCGTACAGGAGGAGCGCCATCTGTGCC							

RESULT 11

US-09-954-456-216
; Sequence 216, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION.

Db	196	AATTTGGTGAATTTCCACAGAATGATCAAGTTGACGACAGGAAGAACCCGACTCACT	255
Qy	121	TTCTGGGCTACGGTTGCTACTGTGGCTGGGGGGCGGTGCCAGCCCAAGGATGAGGTG	180
Db	256	TATGGCTTCTACGGCTGCCACTGTGGGTGGCGAGAGTATCCCCCAAGGATGCAACG	315
Qy	181	GACTGTGTGTGCCACGCCGACGACTGCTCTACCAAGGAATCTTTTGACCAAGGCTGTGAC	240
Db	316	GATCGCTGTGTGTCATCTGCTCATGCTGTTGCTACAAACGCTGGAGAAACGTTGGATGTGGC	375
Qy	241	CCCTA	245
Db	376	ACCAA	380

RESULT 10

```

US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

```

Query Match

Best Local Similarity	11.4%	Score	57.8;	DB	10;	Length	1076;
Matches	128;	Conservative	0;	Mismatches	117;	Indels	0;
						Gaps	0;
1	ATGAAGAAGTTCTTTCACCGTGGCCATCCTTGTCTGGCAGCGTCTCTGCCACAGCTCACGGC	60					
196	ATGAAGACCCCTCTACTGTTGGCAGTCATGATCTTTGGCCTACTCGAGGCCCATGG	255					
61	AGCCTGCTCAACCTGAAGGCCATGTGGAGGCCGTACAGGAGGAGCGCCACTCCTGTCC	120					
256	AATTGTGTGAATTTCCACAGATGATCAAGTTTGACGACAGGAAAGAACCGCCTCAGT	315					
121	TTGCTGGGTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGT	180					
316	TATGGCTTCTACGGCTGGCCACTGTGGCGTGGGTGGCAGAGGATCCCCAAGGATGCAACG	375					
181	GACTGTGTGTCACGCGCCACGACTGCTGCTACACAGAACTTTTGTACCAAGGCTGTAC	240					
376	GATCGGTGTGTGTCACTCATGCTGTGTCTTACAAACGCTCTGGAGAAACGTGATGTGC	435					
241	CCCTA	245					
436	ACCAA	440					

RESULT 11

US-09-954-456-216
; Sequence 216, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION.

QY 155 GCGTGGCCAGCCCCAAGGATGAGTGGACTGGTCGCCACGCCACGACTGCTGCTA 212
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 GCTAGGCACCCCCGTGGATGAAC TGGAACAGTCTGCCACACATGACAAC TGTCA 258

RESULT 14

US-09-925-297-52
Sequence 52, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 630
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (556)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (628)
OTHER INFORMATION: n equals a,t,g, or c
09-925-297-52

Query Match	11.38;	Score	57.2;	DB	10;	Length	630;
Best Local Similarity	67.8;	Presd.	No. 1.3e-06;				
Matches	80;	Conservative	0;	Mismatches	38;	Indels	0;
QY	95	TCACAGGAGGAGCCATCTGCTCTCTGCGGCTACGGTGTGCTACTGTGGCTGGGGG	154				
Db	130	TCCGGGGAGTGACCCCTTTTGGATACAACAACCTACGGCTGCTACTGTGCTTGGGGG	189				
QY	155	GCCGTGGCCAGCCCAAGGATGAGTGGACTGTGTCGCACGCCACGACTGCTGCTA	212				
Db	190	GCTAGGCACCCCGTGGATGACCTGGCAAGTGTGCCAGACACATGACAACCTGCTA	247				

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RESULT 15
US-09-765-231A-42
; Sequence 42, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakamur, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; FILE REFERENCE: vectors, and cells
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 42
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 1-854
; LOCATION: unknown
; OTHER INFORMATION: unsure at all n locations
US-09-765-231A-42

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Query Match	10.8%	Score 55	DB 10	Length 854
Best Local Similarity	53.5%	Pred. No. 5.8e-06		
Matches 115	Conservative	0	Mismatches 100	Indels 0
QY	1	ATGAAGAAGTCTTTCACCGTGGCCATCCTTGCTGGCAGCGTCTGTGCCACAGCTCAGGC	0	Gaps
Db	149	ATGAAGACCCCTCTACTGTTGGCAGTGATCATGATCTTTGGCCTACTGGCCCATGGG	0	
QY	61	AGCCTGCTCAACCTGAAGGCCATGTGTGGAGCGGCTCACAGGAGGAGGCCCATCTCTGTGCG	0	
Db	209	AATTTGGTGAATTTCCACAGAATGATCAAGTTCCAGCAGAGAAAGAACGCCCACTCACT	0	
QY	121	TTGCTGGGCTACGGTTGTCTACTTGGGCTGGGGGCGGTGGCCAGCCCAAGGATCAGGTG	0	
Db	269	TATGGCTTCTACGGTGGCACTTGCGCTGGGTGGCAGAGATCCCCCAAGSATCAACG	0	
QY	181	GACTGGTCTGCCAGGCCACGACTGCTGTACCA	215	
QY	329	GATCGCTGCTGTCACTCATGCTGTGCTACAA	363	

Search completed: February 8, 2003, 06:43:54
Job time : 58 secs

GenCore version 5.1.3
Copyright (C) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 02:43:59 ; Search time 1939 Seconds
(without alignments)
4234.715 Million cell updates/sec

Title: US-09-975-456b-1
Perfect score: 507
Sequence: 1 atgaagaagttcttcacgt.....cgccccccgcctccctccctag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba:**
- 2: em_estba:**
- 3: em_estin:**
- 4: em_estin:**
- 5: em_estu:**
- 6: em_estov:**
- 7: em_estpl:**
- 8: em_estro:**
- 9: em_hci:**
- 10: gb_est1:**
- 11: gb_hic:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: gb_gss:**
- 18: em_gss_hum:**
- 19: em_gss_inv:**
- 20: em_gss_pln:**
- 21: em_gss_vrt:**
- 22: em_gss_fun:**
- 23: em_gss_mam:**
- 24: em_gss_mus:**
- 25: em_gss_other:**
- 26: em_gss_pro:**
- 27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	255.4	50.4	657	10	BB613865	BB613865
2	186.4	36.8	511	9	AI173803	AI173803 ue2cc03.y
3	167.8	33.1	486	9	A1931322	A1931322 ul67fi2.y
4	165.2	32.6	484	9	A1574411	A1574411 uk20g11.y
5	146	28.8	452	9	AI173890	AI173890 ue92h04.y
6	138	27.2	455	10	AW106043	AW106043 um22d03.y

7	99.6	19.6	463	13	BM153087
8	99.2	19.6	533	10	AW213414
9	94.6	18.7	484	13	BM106914
10	91.2	18.3	950	12	BF781906
11	91.2	18.0	680	13	B1836812
12	89.2	17.6	392	10	AW659630
13	89.2	17.6	558	13	BM363855
14	88.4	17.4	460	12	BF077514
15	83	16.4	460	9	AI430241
16	82.4	16.3	367	10	BB689347
17	82.4	16.3	472	10	BE138146
18	82.4	16.3	1582	11	AK018005
19	82	16.2	501	9	AA762051
20	81.8	16.1	446	14	BQ570398
21	81	16.0	1206	11	AK004232
22	79.6	15.7	620	9	AL660516
23	79.4	15.7	601	14	BQ418599
24	77.6	15.3	544	10	BE015249
25	75.8	15.0	543	10	AW292929
26	75.8	15.0	558	13	BM087924
27	75.4	14.9	909	12	BG293389
28	73.8	14.6	432	10	BB850720
29	73.6	14.5	442	9	AI769633
30	73.4	14.5	235	10	BE477104
31	71.8	14.2	666	10	AW918786
32	70.2	13.8	323	14	BM688463
33	70.2	13.8	447	14	BM688506
34	70	13.8	233	10	AW418175
35	68.2	13.5	388	12	BF150826
36	68	13.4	428	10	BB849474
37	66.6	13.1	356	10	BB868695
38	65.8	13.0	445	14	N93958
39	65.4	12.9	587	10	BB615766
40	65.4	12.9	834	13	BG964576
41	64.8	12.8	1590	14	BM926265
42	64.4	12.7	381	10	BE128774
43	64.2	12.7	396	10	AV691515
44	64.2	12.7	398	10	AV695929
45	64.2	12.7	410	10	AV698272

ALIGNMENTS

RESULT 1
BB613865
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BB613865 RIKEN full-length enriched, 0 day neonate head Mus
musculus cDNA clone 4831444E21 5', mRNA sequence.
BB613865
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

BB613865.1 GI:153955682

1 (bases 1 to 657)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Kouda,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

TITLE
JOURNAL
COMMENT

BB613865
musculus cDNA clone 4831444E21 5', mRNA sequence.
BB613865
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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location/Qualifiers
1. .657
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4831444E21"
/clone_lib="RIKEN full-length enriched, 0 day neonate
head"
/sex="mixed"
/tissue.type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5', GAGAGAGAGATTCGAGTTATTAATATGCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
vector; a modified pBluescript KS(+) after bulk excision
from lambda phage."

```

BASE COUNT	154 a	188 c	180 g	135 t	
ORIGIN					
Query Match		50.4%;	Score 255.4;	DB 10;	Length 657;
Best Local Similarity		80.8%;	Pred. No. 2.1e-53;		
Matches 298;		Conservative	0;	Mismatches 71;	Indels 0; Gaps 0;
1	ATGAAGAAGTTTTCACCGTGGGCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC	60			
QY					
239	ATGAAGAAATTTTGGCATCGGAGTCTCTGGCGGAGTGTGTAAACACGCGCCACAGC	298			
DB					
61	AGCCTGCTAACCTCAAGGCCATGGTGGAGCGGTACACAGGAGGAGCGCCATCCTGTCC	120			
QY					
299	AGCCTGCTGAACCTGAAGTGCATGGTGGAGGCCATCACACAGAAACATCCATTCCTGTCC	358			
DB					
121	TTCTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTGGCCAGCGCCCAAGGATGAGGTG	180			
QY					

359	Db	TTTGTGGGCTACTGCGGCTGCTACTGCGGCTGGGGGACGGCGGCATCCATGGATGAGTTA	418
181	Qy	GACTGTGCTGCCAGCCAGCACTGCTGTACACGAACTCTTTTGACCAAGCCTGTCAAC	240
419	Db	GACTGGTCTGCCATGCCCAGCACTGTTGCTATGAGAGCTCTTTGAGCAGGCTGCCGC	478
241	Qy	CCCTATGTGGACCACTATGATCACCACCTGAGAACCACTAGATAGTCTGCAGTGC	300
479	Db	CCCTACGTGGACCACTATGATGACCAAGATCGAAATGCACCATGATGTCTGCACATGAG	538
301	Qy	CTCACACAGACAGATGTGACAAAGCAGACATGCATGTGTGACAAAGACATGGTTCTGTGC	360
539	Db	CTCAATGACGAGGATGTGTGACAAAGCAAAATGCCAGTGTGACAGAGCCTCCCTCTGTGC	598
361	Qy	CTCATGAAC	369
599	Db	CTAAGGATC	607

RESULT 2	511 bp	mRNA	linear	EST 07-OCT-1998
AI173803	ue92c03.y1	Sugano mouse embryo mewa	Mus musculus	CDNA clone
LOCUS	IMAGE:1498564	5', similar to SW:PA24_RAT P39878	14 KD PHOSPHOLIPASE	
DEFINITION	A2 PRECURSOR ;	mRNA sequence.		
ACCESSION	AI173803			
VERSION	AI173803.1	GI:3719945		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 511)			
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,			
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,			
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,			
	Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and			
	Waterston,R.			
TITLE	The WashU-HMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	Contact: Marra M/Mouse EST Project			
	WashU-HMI Mouse EST Project			
	Washington University School			
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: mouseest@watson.wustl.edu			
	This clone is available royalty free through LLNL; contact the			
	IMAGE Consortium (info@image.llnl.gov) for further information.			
	MG1:936168			
	Possible reversed clone: similarity on wrong strand			
	Seq primer: custom primer used			
	High quality sequence stop: 442.			
FEATURES	Location/Qualifiers			
source	1. 511			
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	/strain="C57BL"			
	/db_xref="taxon:10090"			
	/clone="IMAGE:1498564"			
	/clone_lib="Sugano mouse embryo mewa"			
	/dev_stage="embryo, 14 dpc"			
	/lab_host="DH10B"			
	/note="vector: (PME18S-FL3; Site_1: DraIII (CACTGTTGTG);			
	Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed			
	with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTT];			
	double-stranded cDNA was ligated to a DraIII adaptor			
	[TGTGTGGCCTACTGS], digested and cloned into distinct DraIII			
	sites of the PME18S-FL3 vector (5' site CACTGTGTG, 3' site			
	CACCATGTG). XhoI should be used to isolate the cDNA			
	insert. Size selection was performed to exclude fragments			
	<1.5Kb. Library constructed by Dr. Sumio Sugano			
	(University of Tokyo Institute of Medical Science).			
	Custom primers for sequencing: 5' end primer			


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/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1498615"
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/lab_host="DH10B"
/note="vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TTGTGGCCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAGCTGCG and 3' end primer
CGACTCGAGCTCGAGCACA."
BASE COUNT      97 a 137 c 129 g      89 t
ORIGIN
Query Match      28.8%; Score 146; DB 9; Length 452;
Best Local Similarity 82.7%; Pred. No. 3.8e-26;
Matches 167; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGAAGAAGTTCTTCCACCTGGCCATCTTGTGTCGACGGTCTCTCCACAGCTCACGGC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 ATGAAGAAATTTCTTCCATCGCAGTCTCTGGCGGCGAGTGTGTAACACGCCGCCACAGC 310
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AGCTGCTCAACTGAAGCCATGTGGAGCGGCTACACAGGAGAGCGCCATCTCTGTCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 AGCTGCTGAACCTGAAGTCCATGTGGAGGCCATCACACAGAAATCTCATCTGTGCC 370
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 TTCTGGGCTACGGTGTCTACTGTGGGCTGGGGCGGCTGGCCAGCCCAAGATGAGGTG 180
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Db 371 TTCTGGGCTACGGTGTCTACTGTGGGCTGGGGGACGCCGCATCCATGATGAGGTA 430
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GACTGTGTGCCACGCCACGCCACG 202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 GACTGTGTGCCATGCCACGCCACG 452

RESULT 6
AW106043 455 bp mRNA linear EST 20-OCT-1998
LOCUS um22d03.y1 Sugano mouse embryo meva Mus musculus cDNA clone
DEFINITION IMAGE:2225285 5' similar to TR:042187 042187 PHOSPHOLIPASE A2 ;
      mRNA sequence.
ACCESSION AW106043.1 GI:6076779
VERSION AW106043
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 452)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Underwood, K., Kucaba, R., Theising, B., Harven, M., Bowers, Y., Person
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-HHMI Mouse EST Project 1999
Unpublished (1996)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
Seq primer: custom primer used.
Location/Qualifiers

FEATURES

```


Mon Feb 10 11:35:50 2003

REFERENCE
AUTHORS
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 533)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1007887
Seq primer: custom primer used
High quality sequence stop: 465.

FEATURES
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Location/Qualifiers
1..533
/organism="Mus musculus"
/strain="C57BL"
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/clone="IMAGE:2259179"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/note="Vector: (PME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CCATGATG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGGCGCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the PME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCGCTCTAAAGCTGCG and 3' end primer
CGACCTGAGCTCGAGCACA."

BASE COUNT 120 a 155 c 146 g 109 t 3 others
ORIGIN
Query Match 19.6%; Score 99.2; DB 10; Length 533;
Best Local Similarity 80.1%; Pred. No. 1.9e-14;
Matches 141; Conservative 0; Mismatches 33; Indels 2; Gaps 2;
QY 1 ATCAAGAGTTCTACCGTGGCCATCTTGTGTCGAGCGTCTGTCCACAGCTCACGGC 60
Db 246 ATGAAGAAATCTTTCGATCGGAGTCTTGGCGGAGTGTGTTACACACGCGCCACAGC 305
QY 61 AGCTGCTCAACCTGAAGGCCATCGTGGAGCGCGTCAAGGAGGAGCGGCA-TCTGTGC 119
Db 306 AGCTGCTGAACCTGAAGTCCATGTTGGAGGCCATCACACAGAACTCCATTCCTGTC 365
QY 120 CTTGCTGGGCTAGGTTGCTACTGTGGCTGGG-GGCGCTGGCCAGCCCAAGGAT 174
Db 366 CTTTGTGGGCTAGGCTGCTACTGTGGGCTGGGNGGACCGCGCCATCCCATGGAT 421

RESULT 9
BM106914 484 bp mRNA linear EST 21-NOV-2001
LOCUS
DEFINITION 510989 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM106914
VERSION BM106914.1 GI:17037984
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE
AUTHORS
Bovidae; Bovinae; Bos.
1 (bases 1 to 484)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keeler, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTITCCAGTCACGAGC
Plate: 104 row: K column: 22
Seq primer: ATTTAGGTGACATATAG.

FEATURES
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Location/Qualifiers
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/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 101 a 146 c 131 g 106 t
ORIGIN
Query Match 18.7%; Score 94.6; DB 13; Length 484;
Best Local Similarity 58.2%; Pred. No. 2.6e-13;
Matches 188; Conservative 0; Mismatches 129; Indels 6; Gaps 1;
QY 40 GTTCTGCCAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGTTGGAGCGCGTCACA 99
Db 62 GGTGTGGCTCCAGCGGAGCGGACATCTGACCTGAACAGAGTGGTCAGACAAGTCACG 121
QY 100 GGGAGGAGCGGCATCTCTCTGTTGGGTACCGTGTGCTGTTGCTGGGGCGCGT 159
Db 122 GGAAGATCCCATCTCTCTTATTCACATATGCTGTTACTGCAGAAAAGGTGGCCAA 181
QY 160 GGCCAGCCCAAGGATGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
Db 182 GGCCAAACCCAGAGATGCCACAGACAGGTGCTGCGGTGACCATGATGCTGCTACCGTAC 241
QY 220 CTTCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCATACCATCGAACAAC 279
Db 242 CTGAATCTGACAACTGTGACATAGCTTCGACCACTATGACTACACCTT-----TTTC 295
QY 280 ACTGAGATAGTGTGAGTGACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGT 339
Db 296 CAGGGGAAATCCAGTGTGTTCCACCAAGGGGAGCTGTTGAGCAGCAGCATGTGCGCCCTGT 355
QY 340 GACAAGACATGTTCTGTGCT 362
Db 356 GACAAGACGTTGGCCTTCTGCT 378

RESULT 10
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LOCUS
DEFINITION 602105856F1 NCI_CGAP_K1d14 Mus musculus cDNA clone IMAGE:4234596
5', mRNA sequence.

Qy	167	CCAAGGATGAGTGGGACTGGTGTGCCACGCCACGACTGCTACCAAGGAACCTTTG	226
Db	225	CCCAGGATGCTATAGACTGGTGTGCCATGCGCAGCACTGCTGCTATACACATGCCGAGA	284
Qy	227	ACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCATCGAGACAACACTGAGA	286
Db	285	ACTCCGGCTGCAATCCCAAGTGCACCCCT-----ACTCCTGGGAATTGTGTCAGTCAAGA	338
Qy	287	TAGTCTGCAGTGACCTCAACAAGACAGAGTGTGCACAGCAGACATGCATGTGTGACAAGA	346
Db	339	GTGTCAAGTGTGAACCAACGGAGGACAAATGCCAAGAACTCATATGCAAGTGTGACCAGG	398
Qy	347	ACATGGTTCGTGTGCCTCATGAACCAAGACGTACCGAGAGGAGTACCGTGCCTTCCTCAATG	406
Db	399	AGTTTGCTCACTGCTTATAGCCCGAGCAGAGTACACAACTTAAGTACCTCTTCTATCCCCATT	458
Qy	407	TCCTACTGCCAGGGCCCCACGCCCAACTG	434
Db	459	TCCTGTGTGGGAACACTACTCACCCGAGT	486

LOCUS	AI430241	460 bp	mRNA	linear	EST 09-MAR-1999
DEFINITION	vv49h02.y1 Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:1225779 5' similar to SM:P42M_CAVPO P47711 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR ; , mRNA sequence.				
ACCESSION	AI430241				
VERSION	AI430241.1	GI:4276077			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
TITLE	Unpublished (1997)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:651371				

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FEATURES
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        /clone_lib="Soares_thymus_2NbMT"
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        /tissue_type="Thymus"
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        /lab_host="DH10B"
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was primed with a Not I - oligo(dt) primer [5,
TGTTACCAACTGTGAAGTGGGAGCGCGCGTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
      119 a 123 c 123 g 94 t 1 others

```

Mon Feb 10 11:35:50 2003

Query Match 16.4%; Score 83; DB 9; Length 460;
 Best Local Similarity 54.2%; Pred. No. 2e-10;
 Matches 192; Conservative 0; Mismatches 156; Indels 6; Gaps 1;

QY 39 CGTTCCTGCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGCTCAC 98
 Db 3 CGGTATTAACCTGCAACCCAGGGAGGGCTCCTGAACCTGAACAGATGGTCACACACATGAC 62

QY 99 AGGGAGGAGCGCCATCCTGTCTTCCTGCTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGG 158
 Db 63 GGGGAAGAAAGCCCTTCTTCAGCTACTTGGCCCTACGGCTGTCTACTGTGAGCTTGGTGGCAA 122

QY 159 TGGCCAGCCCAAGGATCAGGTGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
 Db 123 AGGGCAACCCAAAGATGCCACAGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 182

QY 219 ACTCTTTGACCAAGGCTGTCAACCCCTATGTGGACCTATGTATGATCACACCATCGAGAACA 278
 Db 183 CCTGAAGATCGTGGATGCAAGAGCCCTGACAGACAACACTACAATACAGCATCTCCAGGG 242

QY 279 CACTGAGATAGTGTGCAAGTCAACCTCAACAAGACAGAGTGTGACAAGCAGACATGCAATGTG 338
 Db 243 CACT-----ATCCAGTGTCTGACAAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTG 296

QY 339 TGACAAGAACATGGTTCCTGTGCTCTGACCAACAGAGCTACCCGAGAGGAGTACCG 392
 Db 297 TGACAAGGAGGTGGCCTTGTGTGTAAGCAAAACCTGNATAGCTACAATAAGCG 350

Search completed: February 8, 2003, 05:46:24
 Job time : 1947 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:27 ; Search time 36 Seconds
(without alignments)
621.836 Million cell updates/sec

Title: US-09-975-456b-2

Perfect score: 957

Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	211	23	Human lipid metabo
2	353	36.9	145	22	Novel human protei
3	352	36.8	145	21	Human secretory ph
4	352	36.8	145	21	Human phospholipas
5	352	36.8	145	22	Human CG95 (or C87
6	352	36.8	145	22	Human EST encoded
7	352	36.8	150	22	Human protein sequ
8	344.5	36.0	144	21	Mouse secreted pho
9	344.5	36.0	144	21	Mouse secretory ph
10	313.5	32.8	142	21	Mouse secretory ty

11	313.5	32.8	142	22	AAB81021	Murine phospholipa
12	309	32.3	142	22	AAB81022	Human phospholipas
13	302.5	31.6	144	10	AAP93363	Human synovial pho
14	302.5	31.6	144	10	AAP93112	Human inflammatory
15	302.5	31.6	144	13	AAR25416	PLA2. Synthetic.
16	302.5	31.6	144	16	AAR34055	Human PLA2 type II
17	302.5	31.6	164	21	AAB56432	Human prostate can
18	284.5	29.7	122	21	AAV88292	Agkistrodon sp. PL
19	283	29.6	146	18	AAW08368	Mouse PLA2s (wildt
20	283	29.6	146	23	ABB08154	Murine PLA2 enzyme
21	282.5	29.5	151	23	ABB08084	Mouse x-type secre
22	282.5	29.5	151	23	AAW49005	Mouse x-type secre
23	278	29.0	125	16	AAR63060	Rat PLA2 type II.
24	277	28.9	145	16	AAR63053	HPLA2-8. Homo sap
25	275.5	28.8	124	12	AAW10126	Membrane-bound pho
26	275.5	28.8	124	20	AAW73562	Human group II sec
27	275.5	28.8	138	16	AAR63046	HPLA2-10. Homo sa
28	273.5	28.6	116	21	AAW24434	Human PRO1561 prot
29	273.5	28.6	116	21	AAW99450	Human PRO1561 (UNQ
30	273.5	28.6	116	22	AAU12438	Human PRO1561 poly
31	273.5	28.6	116	22	AAB66199	Protein of the inv
32	272.5	28.5	137	16	ABW08155	Murine PLA2 enzyme
33	268.5	28.1	137	13	AAR63045	RPLA2-10. Rattus
34	268.5	28.1	155	23	ABB80081	Human x-type secre
35	268.5	28.1	135	23	AAW49002	Human x-type secre
36	268.5	28.1	165	20	AAW07481	Human phospholipas
37	268.5	28.1	165	23	ABB80080	Human secretory ph
38	268.5	28.1	165	23	AAW49001	Human x-type secre
39	267	27.9	158	16	AAR63044	RPLA2-8. Rattus s
40	264.5	27.6	118	20	AAW99582	Solid phase sequen
41	257	26.9	478	22	ABG27553	Novel human diagno
42	246.5	25.8	132	19	AAW58476	Human synovial flu
43	236.5	24.7	122	14	AAR39346	Phospholipase A2 s
44	228	23.8	145	11	AAW04821	D-helix deficient
45	225.5	23.6	145	21	AAW88294	Bovine PLA2 protei

ALIGNMENTS

RESULT 1
ABB08202
ID ABB08202 standard; Protein; 211 AA.
AC ABB08202;
XX
XX
DT 04-MAR-2002 (first entry)
XX
XX
DE Human lipid metabolism enzyme-2 (LME-2).
KW Human; LME-2; lipid metabolism enzyme-2; cytosolic; neuroprotective;
KW immunosuppressive; anti-inflammatory; cardiovascular; gene therapy;
KW enzyme therapy; cancer; neurological disorder; autoimmune disorder;
KW inflammatory disorder; cardiovascular disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200185956-A2.
XX
XX
PD 15-NOV-2001.
XX
XX
PF 11-MAY-2001; 2001WO-US15210.
XX
XX
PR 11-MAY-2000; 2000US-203511P.
PR 25-MAY-2000; 2000US-207903P.
PR 07-JUN-2000; 2000US-210150P.
PR 23-JUN-2000; 2000US-213392P.
XX
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX
PI Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;

SEQ ID NO 12
of the publication
table 2


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XX SQ Sequence 145 AA;
Query Match 36.9%; Score 353; DB 22; Length 145;
Best Local Similarity 45.5%; Pred. No. 3.7e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYCGGLGGRCQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLCGLVWAGVPIPTGGILNLKMKVKQVTGKMPILSWPYGCHGGLGGRCQPKDATDW 62

QY 63 CCHAHCCVQELFDQCHPYVDHYDHTIENNTFIVCSDLNTECDKQTCMCDKKNVLCLM 122
   || ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 63 CCQTHDCCYDHLTKQCGSIYKDYRYNFSQ- NIHCSD- KGSWCQQLCACDKEVAFCLK 120

QY 123 N--QTYREEYRGFLNVYCGPTPNC 145
   ||:: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 121 RNLDTYQKRLRFYWRPHCRGQTGPGC 145

RESULT 3
AAB12537
ID AAB12537 standard; Protein; 145 AA.
AC AAB12537;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human secretory phospholipase A2 protein sequence SEQ ID NO:27.
XX
KW Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW antibacterial; immunosuppressive; tranquilizer; vulnerary;
KW antirheumatic; antiarthritic; septic shock; trauma; pancreatitis;
KW allergic rhinitis; chronic rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= signal
FT Protein 21..145
FT /label= PLA2
XX
PN WO200034486-A1.
XX
PD 15-JUN-2000.
XX
PF 07-DEC-1999; 99WO-JP06844.
XX
PR 09-DEC-1998; 98JP-0349608.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Ishizaki J, Suzuki N, Hanasaki K;
DR WPI; 2000-423429/36.
DR N-PSDB; AAA60878.
XX
PT Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT diagnosis and treatment of secretory PLA2-associated diseases e.g.
PT septic shock, trauma, pancreatitis, allergic rhinitis and chronic
PT rheumatoid arthritis.
XX
PS Claim 1; Page 41; 45pp; Japanese.
XX
CC The present invention describes human secretory phospholipase A2 (PLA2).
CC PLA2 has antiallergic, antiinflammatory, antibacterial, tranquilizer,
CC immunosuppressive, vulnerary, antirheumatic and antiarthritic
CC activities. Human secretory phospholipase A2 (PLA2), the gene encoding
CC it and antibodies against it are useful for the diagnosis and treatment
CC of secretory PLA2-associated diseases e.g. septic shock, trauma,
CC pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC present sequence represents human PLA2.
```

```
XX SQ Sequence 145 AA;
Query Match 36.8%; Score 352; DB 21; Length 145;
Best Local Similarity 45.5%; Pred. No. 4.6e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYCGGLGGRCQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLCGLVWAGVPIPTGGILNLKMKVKQVTGKMPILSWPYGCHGGLGGRCQPKDATDW 62

QY 63 CCHAHCCVQELFDQCHPYVDHYDHTIENNTFIVCSDLNTECDKQTCMCDKKNVLCLM 122
   || ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 63 CCQTHDCCYDHLTKQCGSIYKDYRYNFSQ- NIHCSD- KGSWCQQLCACDKEVAFCLK 120

QY 123 N--QTYREEYRGFLNVYCGPTPNC 145
   ||:: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 121 RNLDTYQKRLRFYWRPHCRGQTGPGC 145

RESULT 4
AAB03627
ID AAB03627 standard; protein; 145 AA.
XX
AC AAB03627;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human phospholipase 1 HPPL1.
XX
KW Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= putative_signal_peptide
FT Peptide 1..16
FT /label= putative_signal_peptide
FT Protein 17..145
FT /label= putative_mature_HPPL1
FT Active-site 21..145
FT /label= phospholipase_A2_active_site_signature
FT Protein 22..145
FT /label= putative_mature_HPPL1
FT Modified-site 33
FT /label= potential_phosphorylation_site
FT Region 44..92
FT /label= active_site_histidine_region
FT Region 88..140
FT /label= active_site_aspartic_acid_region
FT Modified-site 89
FT /label= potential_glycosylation_site
FT Modified-site 98
FT /label= potential_phosphorylation_site
FT Modified-site 102
FT /label= potential_phosphorylation_site
XX
PN WO200024911-A2.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US25021.
XX
PR 27-OCT-1998; 98US-0181317.
PR 21-JAN-1999; 99US-0234726.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI Asimzai Y, Lal P, Lu DAM;
XX
```


Mon Feb 10 11:36:14 2003

QY 123 N--QTYREYRGFLNVYCOGPTNC 145
 Db 126 NLDYTKRLRFLYWRPHCRGQTPGC 150

RESULT 8
 AAB11994
 ID AAB11994 standard; Protein; 144 AA.

XX AAB11994;
 XX 24-NOV-2000 (first entry)
 DT Mouse secreted phospholipase A2.
 DE Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
 KW antibody; diagnosis; drug screening; expressed sequence tag; EST.
 KW Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT Protein /note= "Signal peptide"
 FT Protein 20..144
 FT Protein /note= "Mouse mature secreted phospholipase A2"

XX JP2000166544-A.
 XX 20-JUN-2000.
 XX 09-DEC-1998; 98JP-0349602.
 XX 09-DEC-1998; 98JP-0349602.
 XX (SHIO) SHIONOGI & CO LTD.
 XX WPI; 2000-458171/40.
 XX N-PSDB; AAA72076.

XX Mouse secretion type phospholipase A2 -
 PS Claim 1; Page 10-11; 12pp; Japanese.

XX This sequence represents a mouse secreted phospholipase A2 (secreted PLA2). A cDNA was initially identified in an EST (expressed sequence tag) database, and a fragment (AAA72077) was isolated from cDNA derived from several mouse tissue types using primers AAA72078-A72081. The full length cDNA was generated using primers AAA72082-A72088. The invention relates to the novel secreted PLA2, nucleic acids encoding it, and variants of the protein which retain phospholipase A2 activity. It also encompasses an expression vector and host cells comprising DNA encoding murine secreted PLA2, a method for the recombinant production of the protein, a method of screening potential inhibitors of the protein and the compounds thus identified, and an antibody specific for murine PLA2. The antibody can be used for the diagnosis of a variety of diseases.

XX Sequence 144 AA;
 Query Match 36.0%; Score 344.5; DB 21; Length 144;
 Best Local Similarity 45.1%; Pred. No. 2.3e-24;
 Matches 65; Conservative 20; Mismatches 52; Indels 7; Gaps 4;

QY 7 VAILAGSVL---STAHGSLNLLKAMVEAVTGRSAILSFVGYGCGLGGRGPKDEVDWC 63
 Db 3 LALLCGLLAGITATOGGLLNLLNKVYTHMTGKKAFFSWPYGCHGGLGGKQPKDADWC 62

QY 64 CHAHDCCYOELFDQGHYPYVDHYDHTIENNTFVCSDLNKTCDKQTCMCKNNVLCIMN 123
 Db 63 CQKHDCCYAHLKIDGCKSLTDNFKYSISQGT-IQCSN-NGSWCERQLCACDKEVALCLIKQ 120

QY 124 --QTYREYRGFLNVYCOGPTNC 145
 Db 121 NLDYTKRLRFLYWRPHCRGQTPAC 144

RESULT 9
 AAB12536
 ID AAB12536 standard; Protein; 144 AA.

XX AAB12536;
 XX 02-NOV-2000 (first entry)
 DT Mouse secretory phospholipase A2 protein sequence SEQ ID NO:14.
 DE Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
 KW antibacterial; immunosuppressive; tranquilizer; vulnerary;
 KW antirheumatic; antiarthritic; septic shock; trauma; pancreatitis;
 KW allergic rhinitis; chronic rheumatoid arthritis.

XX Mus musculus.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT Protein /label= signal
 FT Protein 20..144
 FT Protein /label= PLA2

XX WO200034486-A1.
 XX 15-JUN-2000.

XX 07-DEC-1999; 99WO-JP06844.
 XX 09-DEC-1998; 98JP-0349608.

XX (SHIO) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanasaki K;
 XX WPI; 2000-423429/36.
 XX N-PSDB; AAA60866.

XX Human secretory phospholipase A2 (PLA2) and its encoded gene for
 PT diagnosis and treatment of secretory PLA2-associated diseases e.g.
 PT septic shock, trauma, pancreatitis, allergic rhinitis and chronic
 PT rheumatoid arthritis -

XX Example 3; Page 37; 45pp; Japanese.

XX The present invention describes human secretory phospholipase A2 (PLA2).
 CC PLA2 has antiallergic, antiinflammatory, antibacterial, tranquilizer,
 CC immunosuppressive, vulnerary, antirheumatic and antiarthritic
 CC activities. Human secretory phospholipase A2 (PLA2), the gene encoding
 CC it and antibodies against it are useful for the diagnosis and treatment
 CC of secretory PLA2-associated diseases e.g. septic shock, trauma,
 CC pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
 CC present sequence represents mouse PLA2, which is used in an example from
 CC the present invention.

XX Sequence 144 AA;

Query Match 36.0%; Score 344.5; DB 21; Length 144;
 Best Local Similarity 45.1%; Pred. No. 2.3e-24;
 Matches 65; Conservative 20; Mismatches 52; Indels 7; Gaps 4;

QY 7 VAILAGSVL---STAHGSLNLLKAMVEAVTGRSAILSFVGYGCGLGGRGPKDEVDWC 63
 Db 3 LALLCGLLAGITATOGGLLNLLNKVYTHMTGKKAFFSWPYGCHGGLGGKQPKDADWC 62

QY 64 CHAHDCCYOELFDQGHYPYVDHYDHTIENNTFVCSDLNKTCDKQTCMCKNNVLCIMN 123
 Db 63 CQKHDCCYAHLKIDGCKSLTDNFKYSISQGT-IQCSN-NGSWCERQLCACDKEVALCLIKQ 120

QY 124 --QTYREYRGFLNVYCOGPTNC 145
 Db 121 NLDYTKRLRFLYWRPHCRGQTPAC 144

DE Human phospholipase A2 (PLA2) amino acid sequence.

XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary;

KW antiinflammatory; tranquilizer; antiasthmatic; antiallergic; trauma;

KW antirheumatic; antiarthritic; septic shock; pancreatitis; human;

KW adult respiratory distress syndrome; ARDS; bronchial asthma;

KW allergic rhinitis; rheumatoid arthritis.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

PH 1..19

FT /label= Signal_peptide

FT 20..142

FT /label= Mature_PLA2

FT /note= "Mature phospholipase A2"

XX WO200121775-A1.

PN

XX 29-MAR-2001.

XX

XX 18-SEP-2000; 2000WO-JP06344.

XX

XX 21-SEP-1999; 99JP-0266616.

XX

XX (SHIO) SHIONOGI & CO LTD.

PA

PI Ishizaki J, Suzuki N, Hanasaki K;

PI

DR WPI: 2001-290432/30.

DR N-PSDB; AAF77401.

DR

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis

PT of and screening drug candidates for treating associated diseases e.g.

PT septic shock, adult respiratory distress syndrome and rheumatoid

PT arthritis

XX

PS Claim 1; Page 46-47; 50pp; Japanese.

XX

XX This invention relates to human secretory phospholipase A2 (PLA2) protein

CC and the gene encoding it. Inhibitors of phospholipase A2 have

CC antibacterial; immunosuppressive; antiinflammatory; tranquilizer;

CC vulnerary; antiasthmatic; antiallergic; anti-rheumatic; and antiarthritic

CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in

CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult

CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,

CC allergic rhinitis and rheumatoid arthritis. The present sequence

CC represents human PLA2.

XX

SQ Sequence 142 AA;

Query Match 32.3%; Score 309; DB 22; Length 142;

Best Local Similarity 43.8%; Pred. No. 4.5e-21;

Matches 56; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

QY 20 GSLLLKAMVEAVTGRSAILSFGVGYCGYGLGGRQPKDEVWCHAHDCYQLFQGC 79

DB 19 GNLVQFGVMEKMTGKSA-LQYNDYGYCGYGGSHWPVDQTDWCCHAHDCYGRLEKGC 77

QY 80 HPYVDHYDHTIENNTVCSDLNTECDKQTCMCKNMLVCLMQQ--TYREYRGFLNVY 137

DB 78 EPKLEKYLFSV-SERGIFCA--GRTTCORLTCEDCKRAALCFRRNLGTYNKRKYAHYPNKL 134

QY 138 CGQTPNC 145

DB 135 CTGTPPC 142

RESULT 13

AAP93363

ID AAP93363 standard; protein; 144 AA.

XX

AC AAP93363;

27-JUN-1980 (first entry)

XX Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone

DE lambda SPLA2CDNA-4 and by the exons of clone lambda SPLA2-6.

DE

XX Human synovial phospholipase A2; clone lambda SPLA2CDNA-4;

KW lambda SPLA2-6.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

PH 21..144

FT Protein

FT 21..144

PN WO8901773-A.

XX

XX 09-MAR-1989.

PD

XX 23-AUG-1988; 88WO-US02896.

XX

XX 16-AUG-1988; 88US-0231865, US-089883.

XX

XX (BIOT-) BIOTECHN RES PARTN (UTOR).

PA

PI Johnson LK, Seilhamer JJ, Pruzanski W, Vada P;

PI

DR WPI: 1989-085394/11.

DR N-PSDB; AAN91258, AAN91260.

DR

XX Mammalian synovial phospholipase A2- used in food processing

PT design and screening of inflammation inhibitors, as an anticancer

PT drug or vaccine adjuvant etc

PT

XX Fig 6; 70pp; English.

PS

XX Clone lambda SPLA2CDNA-4 is one of four clones identified when probe

CC oligo 2905 (AAN91257) was used to screen a cDNA library constructed from

CC polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2

CC type A sequence which is given here. The mature peptide sequence (see

CC FT) has a calculated molecular weight of 13,919 daltons. The same

CC amino acid sequence is also encoded by the exons of clone lambda

CC SPLA2-6 (AAN91260) in Figure 7.

XX

SQ Sequence 144 AA;

Query Match 31.6%; Score 302.5; DB 10; Length 144;

Best Local Similarity 38.8%; Pred. No. 1.8e-20;

Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

QY 1 MKKFTVAILAGSVLSTAHGSLINLKAMVEAVTGRSAILSFGVGYCGYGLGGRQPKDEV 60

DB 1 MKTLLLLAVIMIFGLLOAHGNLVNFHFMKLTGTGKEAALSYGFYGCYGGVGRGSPKDAT 60

QY 61 DWCHAHDCYQELFQGCYGHVYVDHYDHTIENNTVCSDLNTECDKQTCMCKNMLVCL 120

DB 61 DRCCVTHDCYCKRLEKRGCGTKFLSKYFS-NSGSRITCA--KODSCRSQLCEDKAAATC 117

QY 121 LMNQ--TYREYRGFLNVYCOGTPNC 145

DB 118 FARNTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 14

AAP93112

ID AAP93112 standard; Protein; 144 AA.

XX

AC AAP93112;

XX

XX 31-JUL-1992 (first entry)

XX

XX Human inflammatory phospholipase A2 encoded by HindIII fragment of

DE PLA2 8.5 EMBL3.

XX

Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic; glycerophospholipids; non-pancreatic.
Homo sapiens.

Key Location/Qualifiers
Peptide 1..20
/label= signal
21..39
/note= "Claim 12"
22..37
/note= "Claim 14"
1..14
/label= exon_1
15..62
/label= exon_2
63..98
/label= exon_3
99..124
/label= exon_4
44..56
/note= "calcium binding loop"
68
/note= "calcium binding
67
Active-site
71
FT Active-site
86
FT Active-site
111
W08909818-A.
19-OCT-1989.

11-APR-1989; 89WO-US01418.

15-APR-1988; 88US-0181893.

(BIOJ) BIOGEN INC.

Kramer RM, Pepinsky RB, Hession C;

WPI; 1989-324225/44.

N-PSDB; AAN91825, AAN97209.

Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation of diseases.

Claim 44; Fig 12; 84pp; English.

The protein sequence was deduced from a DNA sequence obt'd. from a genomic DNA library which was prep'd. from a mutant fibroblast cell line which contains 5 copies of the X chromosome (GM5009). The signal sequence is thought to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleotides 5' of this region. The deduced N-terminal sequence of the mature protein confirmed results obt'd. by direct sequencing of the purified protein. This sequence represents an amphiphilic alpha-helix typical of PLA₂ mois. It has highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile (29)] and there is a cluster of basic amino acids [e.g. Arg (27), Lys (30) and Lys (35)] which is believed to be an important determinant in the interaction of PLA₂. There is a characteristic stretch of residues which comprises part of the calcium binding loop: Tyr(44)-Gly-Cys-X-Cys-Gly-X-Gly-X-X-Pro(56) and Asp(68). The conserved residues and the protein exhibits the placement of half-cysteine residues typical of a Gp II PLA₂, having a Cys residue at position 70 and a half cysteine at the C-terminal. (The consensus sequence was determined from a comparison of PUA₂s from bovine pancreas and C. atrox venom.

Sequence 144 AA;

Query Match 31.6%; Score 302.5; DB 10; Length 144;
Best Local Similarity 38.8%; Pred. No. 1.8e-20;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
QY 1 MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSVFGYCYCGLGGRGPKDEV 60
DB 1 MKTLLAVIMIFGLQAHGNLVNHRMIKLTGKREALSFGYCHGCGVGRGSPKDAT 60
QY 61 DMCCHADCCYQELFDQGHYPYVDHYDHTIENNTETVCSDLNKTCDKQTCMCDKNMVL 120
DB 61 DRCCVTHDCCKYRLEKRGCGTFLSYKFS-NSGSRITCA--KODSCRSOLCECDKAAATC 117
QY 121 LMNQ--TYREYRGFLNVCYCGQPTNC 145
DB 118 FARNKTYNKYQYYSNKHCRGSTPRC 144

RESULT 15

AAR25416

ID AAR25416 standard; Protein; 144 AA.

XX AAR25416;

XX 06-JAN-1993 (first entry)

XX PLA2.

Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
erythroid cells; cDNA library.

OS Synthetic.

XX GB2251622-A.

XX 15-JUL-1992.

XX 19-DEC-1991; 91GB-0026984.

XX 21-DEC-1990; 90GB-0027917.

XX (ICIL) IMPERIAL CHEM IND PLC.

PI Antoniou M, Gooding C, Grosveld FG, Hollis M, Needham MRC;

XX WPI; 1992-236158/29.

DR N-PSDB; AAQ26372.

XX Expression vectors for use in mammalian cells - contain dominant control region derived from beta-globin gene

XX Disclosure; Fig 11; 77pp; English.

This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA was amplified using the primer sequences given in AAQ26370-1 by PCR from a human lung cDNA library. The cDNA sequence was used in the construction of an expression vector which further comprised a promoter and a dominant control region. This vector was used in an expression system comprising a mammalian cell transformed with the vector. This expression system could be used to prepare pharmacologically useful polypeptides eg. human growth hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2, and for gene therapy. The mammalian host comprises erythroid cells and a heterologous promoter.

XX Sequence 144 AA;

Query Match 31.6%; Score 302.5; DB 13; Length 144;

Best Local Similarity 38.8%; Pred. No. 1.8e-20;

Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

QY 1 MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSVFGYCYCGLGGRGPKDEV 60
DB 1 MKTLLAVIMIFGLQAHGNLVNHRMIKLTGKREALSFGYCHGCGVGRGSPKDAT 60

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Db 1 MKTLLLVIMIFGLLQAHGNLVNFHRMIKLTGTGKEAALSTGYGCHCGVGRGSPKDAT 60
Qy 61 DWCCCHADCCYQELFDQGCHPYVDHYDHTIENNTIEIVGSDLNKTECDKQTCMCDKNMVL 120
Db 61 DRCCVTHDCCYKLEKXRGCGTKFELSYKFS-NSGSRITCA--KQDSCR SOLCECDKAAATC 117
Qy 121 LMNQ--TYREEYRGFLNVCQGPFPNC 145
Db 118 FARNKTYNKKOYYSNKHCRGSTPRC 144

Search completed: February 10, 2003, 10:36:32
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:31 ; Search time 15 seconds
(without alignments)
329.537 Million cell updates/sec

Title: US-09-975-456b-2

Perfect score: 957

Sequence: 1 MKKFTTVALAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	302.5	31.6	144	1	US-08-186-895-10
2	302.5	31.6	144	2	US-08-888-497-37
3	302.5	31.6	144	4	US-09-362-230-37
4	302.5	31.6	144	5	PCT-US94-07926-37
5	294.5	30.8	146	3	US-08-966-317-4
6	294.5	30.8	146	4	US-09-489-770-4
7	288.5	30.1	146	2	US-08-888-497-35
8	288.5	30.1	146	4	US-09-362-230-35
9	288.5	30.1	146	5	PCT-US94-07926-35
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13	278	29.0	125	4	PCT-US94-07926-42
14	278	29.0	125	5	PCT-US94-07926-42
15	275.5	28.8	124	1	US-08-170-360-4
16	275.5	28.8	124	2	US-08-888-497-39
17	275.5	28.8	124	4	PCT-US94-07926-39
18	275.5	28.8	124	5	US-08-888-497-32
19	275.5	28.8	138	2	US-08-888-497-32
20	275.5	28.8	138	4	US-09-362-230-32
21	275.5	28.8	138	5	PCT-US94-07926-32
22	268.5	28.1	137	2	US-08-888-497-30
23	268.5	28.1	137	4	US-09-362-230-30
24	268.5	28.1	137	5	PCT-US94-07926-30
25	268.5	28.1	165	3	US-08-966-317-1
26	268.5	28.1	165	4	US-09-489-770-1
27	267	27.9	130	2	US-08-888-497-43

28	267	27.9	130	4	US-09-362-230-43	Sequence 43, Appl
29	267	27.9	130	5	PCT-US94-07926-43	Sequence 43, Appl
30	267	27.9	158	2	US-08-888-497-22	Sequence 22, Appl
31	267	27.9	158	4	US-09-362-230-22	Sequence 22, Appl
32	267	27.9	158	5	PCT-US94-07926-22	Sequence 22, Appl
33	264.5	27.6	118	2	US-08-888-497-40	Sequence 40, Appl
34	264.5	27.6	118	4	US-09-097-094-5	Sequence 5, Appl
35	264.5	27.6	118	5	US-09-362-230-40	Sequence 40, Appl
36	264.5	27.6	118	5	PCT-US94-07926-40	Sequence 40, Appl
37	250	26.1	125	1	US-08-170-360-5	Sequence 5, Appl
38	249.5	26.1	117	2	US-08-888-497-44	Sequence 44, Appl
39	249.5	26.1	117	4	US-09-362-230-44	Sequence 44, Appl
40	249.5	26.1	117	5	PCT-US94-07926-44	Sequence 44, Appl
41	237	24.8	124	1	US-08-170-360-1	Sequence 1, Appl
42	236.5	24.7	122	1	US-07-734-534A-1	Sequence 1, Appl
43	225.5	23.6	146	2	US-08-888-497-34	Sequence 34, Appl
44	225.5	23.6	146	4	US-09-362-230-34	Sequence 34, Appl
45	225.5	23.6	146	5	PCT-US94-07926-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Groszfeld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-186-895-10

Query Match 31.6%; Score 302.5; DB 1; Length 144;
Best Local Similarity 38.8%; Pred. No. 8.9e-22;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

RESULT 3
US-09-362-230-37
; Sequence 37, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:

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1  APPLICANT: SERNAMEL, Jelliey
2  TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
3  TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
4  TITLE OF INVENTION: Sequences and Nucleotide Sequences and Nucleotide
5  TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
6  TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
7  NUMBER OF SEQUENCES: 44
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
10 ADDRESSER: Russell PA
11 STREET: 200 East Broward Boulevard
12 CITY: Fort Lauderdale
13 STATE: FL
14 COUNTRY: USA
15 ZIP: 33301
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/362,230

```

```

1 NAME: Manso, Peter J.
2 REGISTRATION NUMBER: 32,264
3 REFERENCE/DOCKET NUMBER: IN21044-5
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 305-527-2498
6 TELEFAX: 305-764-4996
7 INFORMATION FOR SEQ ID NO: 37:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 144 amino acids
10 TYPE: amino acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: protein
14 US-09-362-230-37

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DB 1 MKTLLLLAVIMIFGLLQAGHLNLFHFKMLKLTTCGKAALSIGTFCGCGVGGNGSFRKML 60
QY 61 DWCHAHDCQCYQLFDQGCQPVYDHYDHTIENNTIETVCSDLNTECDKQTCMDCKNNVIC 120
DB 61 DRCCVTHDCCYKLEKRCGKFKLSYKFS--NSGRITCA--KQDSCRSQLCECDKAATC 117
QY 121 LMNQ--TYREERYGFLNVYCQGPNC 145
DB 118 FARNKTTYNNKYQYYSNKHCGRGTPRC 144

RESULT 4
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07926-37

Query Match 31.6%; Score 302.5; DB 5; Length 144;
Best Local Similarity 38.8%; Pred. No. 8.9e-22;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
QY 1 MKKFFTVAILAGSVLSTAHGSLNKLKAMVEAVTGRSAILSFGYCYGCGLGGRGPKDEV 60
Db 1 MKTLLLLAVIMIFGLLQAHGNLVNFRMIKLTGKEAALSYGFYCHGCGVGRGSPKDAT 60
QY 61 DMCHAHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTEDKQTCMCDKNMVLVC 120
Db 61 DRCVTHDCYKRLKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSLCECDKAAATC 117
QY 121 LMNQ--TYREYRGFLNVCYQGPNC 145
Db 118 FARNKTTYNNKYYSNKHCRGSTPRC 144

RESULT 5
US-08-966-317-4
; Sequence 4, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga

; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 204319
US-08-966-317-4

Query Match 30.8%; Score 294.5; DB 3; Length 146;
Best Local Similarity 42.3%; Pred. No. 5.2e-21;
Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;
QY 7 VAILA-GSVLSTAHGSLNKLKAMVEAVTGRSAILSFGYCYGCGLGGRGPKDEVDMCCH 65
Db 9 VVIMAFGSI--QVQSLLEFGQMLFKTKRADVSYGFYCHGCGVGRGSPKDATDMCCV 66
QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTEDKQTCMCDKNMVLCLM--N 123
Db 67 THDCCVNRLEKRGCGTKFLSYKFSRGG-OISCS-TNODSCRKQLCQCDKAAAECEFARNK 124
QY 124 QTYREYRGFLNVCYQGPNC 145
Db 125 KSYSLAYQVFLNKFCKGKTPSC 146

RESULT 6
US-09-489-770-4
; Sequence 4, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.

[illegible]

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35
;
; Query Match 30.1%; Score 288.5; DB 4; Length 146;
; Best Local Similarity 41.5%; Pred. No. 2e-20;
; Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
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; QY 7 VAILA-GSVLSTAAGSLNLKAMVEAVTGRSAILSEFVGYCYGGLGGRGQPKDEVDWCCH 65
; DB 9 VVIMAFGSI--QVQGSLLLEFGQMILFKTKRADVSFGYCHGCGVGRGSPKDATDWCVCV 66
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; QY 66 AHDCCYQELFDQGCCHPYVDHYDHTIENNTTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
; DB 67 THDCCYNRLKRGCGTKFYTKFSYRGG-QISCS-TNODSCRKQLCQCDKAAAEFCFARNK 124
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; QY 124 QTYREYRGFLNVYCOGTPNC 145
; DB 125 KSYSLAYQYPNFKCKGKTPSC 146
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; RESULT 9
; PCT-US94-07926-35
; Sequence 35, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhammer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35
;
; Query Match 30.1%; Score 288.5; DB 5; Length 146;
; Best Local Similarity 41.5%; Pred. No. 2e-20;
; Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
;
; QY 7 VAILA-GSVLSTAAGSLNLKAMVEAVTGRSAILSEFVGYCYGGLGGRGQPKDEVDWCCH 65
; DB 9 VVIMAFGSI--QVQGSLLLEFGQMILFKTKRADVSFGYCHGCGVGRGSPKDATDWCVCV 66
;
; QY 66 AHDCCYQELFDQGCCHPYVDHYDHTIENNTTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
; DB 67 THDCCYNRLKRGCGTKFYTKFSYRGG-QISCS-TNODSCRKQLCQCDKAAAEFCFARNK 124
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; QY 124 QTYREYRGFLNVYCOGTPNC 145
; DB 125 KSYSLAYQYPNFKCKGKTPSC 146
;
; RESULT 10
; US-08-966-317-3
; Sequence 3, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0535
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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us-09-975-456b-2.ra

Mon Feb 10 11:36:15 2003

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;
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;
; US-08-170-360-4

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Query Match      28.8%; Score 275.5; DB 1; Length 124;
Best Local Similarity 39.4%; Pred. No. 2.8e-19;
Matches 50; Conservative 21; Mismatches 51; Indels 5; Gaps 3;

Qy 21 SLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDWCCHADCCYQELFDGCH 80
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 NLVNFHRMIKLTGKEAALSIFYGCHGCGVGGGSPKDATDRCCVTHDCCYKRLEKRGCG 60

Qy 81 PYVDHYDHTIENNTIYVCSLDLNTKTECDKOTCMCDKNMVLIMNQ--TYREYRGFLNVYC 138
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TKFLSYKFS-NSGSRITCA--KQDSRCSQLCECDKAAATCFARNKITYNKKYQYYSNKH 117

Qy 139 QGPTPNC 145
Db 118 RGSTPRC 124

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Search completed: February 10, 2003, 10:37:30
Job time : 15 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	353	36.9	145	9	US-09-969-384-17		Sequence 17, Appl
2	352	36.8	145	10	US-09-935-996A-6		Sequence 6, Appl
3	302.5	31.6	164	10	US-09-925-300-1010		Sequence 1010, Appl
4	294.5	30.8	146	9	US-10-124-591-4		Sequence 4, Appl
5	283	29.6	146	9	US-10-124-591-3		Sequence 3, Appl
6	283	29.6	146	10	US-09-993-999-8		Sequence 8, Appl
7	273.5	28.6	116	9	US-10-038-072-534		Sequence 534, App
8	273.5	28.6	116	9	US-10-121-049-534		Sequence 534, App
9	273.5	28.6	116	9	US-10-123-004-534		Sequence 534, App
10	273.5	28.6	116	9	US-10-140-470-534		Sequence 9, Appl
11	272.5	28.5	137	10	US-09-993-999-9		Sequence 1, Appl
12	268.5	28.1	165	9	US-10-124-591-1		Sequence 5, Appl
13	264.5	27.6	118	9	US-09-987-675-5		Sequence 5, Appl
14	264.5	27.6	118	10	US-09-987-675-5		Sequence 5, Appl
15	220.5	23.0	156	10	US-09-925-297-511		Sequence 511, Appl
16	208.5	21.8	146	10	US-09-993-999-7		Sequence 7, Appl
17	203.5	21.3	143	10	US-09-993-999-10		Sequence 10, Appl
18	141.5	14.8	79	10	US-09-925-297-873		Sequence 873, Appl
19	131	13.7	37	10	US-09-975-374A-14		Sequence 14, Appl

us-09-975-456b-2.rapb

Mon Feb 10 11:36:15 2003

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US-09-835-996A-6
; Sequence 6, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyun
; APPLICANT: Qian, Xiahong
; APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 145
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-835-996A-6

Query Match      36.8%; Score 352; DB 10; Length 145;
Best Local Similarity 45.5%; Pred. No. 1.7e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

Qy 7 VAILAGSVLSTA----HCSLLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGOPKDEVDW 62
Db 3 LALLCGLVVMAGVIPIOGGIILNLKMKVQVTKGKMPILSYWPYCHGCHGLGGRGOPKDATDW 62

Qy 63 CCHAHDCCYQELFDQGHYPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCLM 122
Db 63 CCQTHDCCYDHLKTQGGIYKYDYRNFSGQ-NIHCSQD-KGSWCQEQQLCACDKREVAFCCK 120

Qy 123 N--QTYREYRGFLNYVCOGTPNC 145
Db 121 RNLDTYKRLRFPYWRPHCRGQTGPG 145

RESULT 3
US-09-925-300-1010
; Sequence 1010, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1010
; LENGTH: 164
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-925-300-1010

Query Match      31.6%; Score 302.5; DB 10; Length 164;
Best Local Similarity 38.8%; Pred. No. 6.7e-21;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

Qy 1 MKKFTTVAIIAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGOPKDEV 60
Db 21 MKTLLAVIMIFGLQAGNLVNFHRMIKLTTCKEAALSYFGYCHGCGVGGRGSPKDAT 80

Qy 61 DWCCAHDCCYQELFDQGHYPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCL 120
Db 81 DRCCVTHDCCTHRCLEKCCGCTKFLSYKFS-NSGSRIICA--KQDSCRSQLCECDKAAATC 137

Qy 121 LMNQ--TYREYRGFLNYVCOGTPNC 145
Db 138 FARNKTTYNKKYQVYSNKHCRGSTPRC 164

RESULT 4
US-10-124-591-4
; Sequence 4, Application US/10124591
; Patent No. US20020177208A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; Bandman, Olga
; Guegler, Karl J.
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,591
; FILING DATE: 16-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/966,317
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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US-10-124-591-4

Query Match 30.8%; Score 294.5; DB 9; Length 146;
Best Local Similarity 42.3%; Pred. NO. 3.2e-20;
Matches 60; Conservative 20; Mismatches 55

QY	7	VAILA--GSVLTSTAHSLLNKAMVEAVTGRSAILSFGVCYCGLGGRGKQDEWCCB	65
		: :	
D8	9	VVIMAFGSI--QVOSSLEFQMILFKYTKRADVSYGFTCHCGVGGRSPKDATDWCV	66
		: :	
QY	66	AHDCCYQBELFDQGHPYVDHYDHTIENNTBEIVGSLNTECKDKQTCMCDKNMVLCM--N	121
D8	67	THDCCYNRLEKRCGCTFLTVKFYSYRG--QISCS-TNQDSCHKQCQCDKAACGFARNK	122
		: :	
QY	124	QTYREERYGFLNVYCOGPTPNC	145
		: : :	
D8	125	KSYLSKYQFYLNKFKCKGTSC	146

RESULT 5

US-10-124-591-3
 : Sequence 3, Application US/10124591
 : Patent No. US20020177208A1
 : GENERAL INFORMATION:
 : APPLICANT: Hawkins, Phillip R.
 : Bandman, Olga
 : Guegler, Karl J.
 : Shah, Purvil
 : Corley, Neil C.
 : TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Dr.
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304

CLONE: 584837
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-124-591-3

Query Match 29.6%; Score 283; DB 9; Length 146;
Best Local Similarity 37.1%; Pred. No. 3.6e-19;
Matches 53; Conservative 26; Mismatches 56; Indels

Qy	9	ILAGSVLS-----TAHGSLLNLKAMVEAVTGRSAILSEVGYCCYCGLGRRQPKQDEVDWCC	64
Db	6	LLAASIMAFGSIQVQGNIAQFGEMIRLKTGKRAELSFVYCGHCGLGCGSPKDATDRCC	65
Qy	65	HAHCCQVLEFDQCGHPYVDHYDHTINNTETVCSDLNKTECDKQTCMCDKNMVLCLM--	122
Db	66	VTHDCCYKSLKSGCGTKLLKYKSHQGG-QITCS-ANQNSCKRLCCQCDKAAAEFCARN	123
Qy	123	NOTYREEYRGFLNYVCOGPTPNC	145
Db	124	KKTYSLKYQFYNNMFCRKGKPKK	146

RESULT 6

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US-09-993-999-8
; Sequence 8, Application US/09993999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: HO, I-Cheng
; APPLICANT: Arm, Jonathan P.
; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; TITLE OF INVENTION: Expressed in Th2 Cells
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993,999
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-993-999-8

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Query Match 29.6%; Score 283; DB 10; Length 146;
Best Local Similarity 37.1%; pred. No. 3.6e-19;
Matches 53; Conservative 26; Mismatches 56; Indels

QY	9	ILAGSVLS- ---TARGSLLNKANWEAVTGRTAIIISFVGYCYCGLGGRGPKDEVDWCC	64
D8	6	LLAASIMAFSGIQVGNIAFGEMIBLKTKRAELUSAFYCHGCLGGKGSPPKDTRCC	65
QY	65	HAHDCCYQLFDQCCHPYVDHYDHTIENNTTESSDLNKTCECDKQTCMCKDNMVLCLM--	122
D8	66	VTHDCCYKLEKSGCGFKLLKYKSHOQG-QITCS-ANQNSCARLCCQDKAAAECAFARN	123
QY	123	NOTREERYRGLNVYCGGPTPNC	145
D8	124	RKTSYLAKYQFYPNMFCKGRKKPC	146

RESULT. T 7

US-10-028-072-534
 : Sequence 534, Application US/10028072
 : Publication No. US20030004311A1
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Beresini, Maureen
 : APPLICANT: DeForge, Laura
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Fillyaroff, Ellen
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Sherwood, Steven
 : APPLICANT: Smith, Victoria
 : APPLICANT: Stewart, Timothy A.

Mon Feb 10 11:36:15 2003

us-09-975-456b-2.rapb

APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028.072
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
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PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/98-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDM 62
3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATDW 62
63 CCHAHDCCYQELFQDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVLCLM 122
63 CCQTHDCCYDHLKTQGGIYKDN-----NKSSIHCDLSQRYC-----LMAVF 105
123 NQTYRE 128
106 NVIYLE 111

RESULT 8

US-10-121-049-534
Sequence 534, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-534

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDM 62
3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATDW 62
63 CCHAHDCCYQELFQDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVLCLM 122
63 CCQTHDCCYDHLKTQGGIYKDN-----NKSSIHCDLSQRYC-----LMAVF 105
123 NQTYRE 128
106 NVIYLE 111

RESULT 9

US-10-123-904-534
Sequence 534, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-534

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY	7	VAILAGCSVLSTA----	HGSLILNKAMVEAVTGRSAILSFVGYCYGCLGGRGQPKDEVDW	62
		..:..:..:	..:..:..:	
Db	3	LALLCGLVWAGVPI	TOGGLILNKNMKVQVTKMFIILSYFPYGCGLGGRGQPKDATDW	62
		..:..:..:	..:..:..:	
QY	63	CGHAHDCCYQELFDQ	GCHPXYDHYDHTIENNTIEIVCSDLANKTECDKQTCMCDKNVVLCLM	122
		..:..:..:	..:..:..:	
Db	63	CCQTHDCCYDLHKT	QGGGIIYKDN-----NKSSIHCMDSLQRYC-----LMAYF	105
QY	123	NOTYRE	128	
		..:..:..:	..:..:..:	
Db	106	NVIIYLE	111	
		..:..:..:	..:..:..:	

RESULT 10
 US-10-140-470-534
 ; Sequence 534, Application US/10140470
 ; Publication No. US20030022331A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C160
 ; CURRENT APPLICATION NUMBER: US/10/140,470
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 534
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-470-534

Query Match	28.6%	Score	273.5	DB	9	Length	116
Best Local Similarity	42.9%	Pred. No.	2.le-18				
Matches	54	Conservative	15	Mismatches	36	Indels	21
Gaps							
3:							
Qy	7	VAILAGSVLSTA----	HGSLNLKAMVAVT	GRSAILSFVGYCYGCLGGRGQPKD	VDM	62	
		: : :	: : :	: : :	: : :	: : :	: :
Db	3	LALLGLVVMAGVIPTGGILNLKRMKVQTKMPILSYFPYGC	HGCLGGRGQPKDATDM	62			
		: : :	: : :	: : :	: : :	: : :	: :
Qy	63	CCHAHDCCYQLFDDQCHPYVDHYDHT	TENNTEIVCSDLANKTECDKOTCMCDKNMVLCLM	122			
		: : :	: : :	: : :	: : :	: : :	: :
Db	63	CCOOTHCCCYDHLKTKQCGIYKDN-----	NKSSIHCMDSLQRYC-----	LMAVE	105		
		: : :	: : :	: : :	: : :	: : :	: :
Qy	123	NOTYRE	128				
		: :	: :				
Db	106	NVIYLE	111				
		: :	: :				

RESULT 11
US-09-993-999-9
; Sequence 9, Application US/09993999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Arm, Jonathan P.

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; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993.999
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246.316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
; OS-09-993-999-9
US-09-993-999-9

Query Match          28.5%; Score 272.5; DB 10; Length 137;
Best Local Similarity 37.9%; Pred. No. 3.1e-18;
Matches 53; Conservative 21; Mismatches 61; Indels 5; Gaps

QY      1 MKKFFTVAILAGSVLSTAHGSLNLNKAMVEAVTGRSAILSFSVGYGCYCGLGGRGQPKDEV 60
       11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MGGLLTFLAWFLACSPVAPVGGLLELSMTKEVTRKNAFKNFYCYCGWGGRGTPKDG 60
       11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DWCCHAHDCQQELFDQGCHPYVDVHDHTIENNTETVCSDLNKTCECDKOTCMCDKNNVLC 120
       1111 11 : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 DMCQCQHRCRQGLEEKDKCAIRTSQSYDIYRTNGL--VICE--HDFCPMRLLCADCRLVYC 117
       1111 11 : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      121 LMNQ--TYREYRGFLNVYC 138
       11 11 : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118 LRNNLTWTYNPLVYQYPNPLC 137
       11 11 : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 12
US-10-124-591-1
; Sequence 1, Application US/10124591
; Patent No. US20020177208A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; Bandman, Olga
; Guegler, Karl J.
; Shale, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,591
; FILING DATE: 16-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/966,317
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVAUTUT01
CLONE: 816403
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-124-591-1

Query Match 28.1%; Score 268.5; DB 9; Length 165;
Best Local Similarity 34.8%; Pred. No. 8.9e-18;
Matches 47; Conservative 23; Mismatches 62; Indels 3; Gaps 3;
QY 11 AGSVLSTANGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDC 70
DB 33 ASRILVRHRRGILEAGTVGCGPRTP1-AYMKYGCFCGLGGHQPRAIDWCCHGHDC 91
QY 71 YQELFDQGGHPYVDHYDHTIENNTIEVCSDLNKTCDKQTCMCKNMVLCMLNQTYREY 130
DB 92 YTRAEEAGGSPKTERYSNQCYNQS-VLCGPA-ENKQELCKCQDEANCLAQTEYNLKY 149
QY 131 RGLNVYCGQPTPNC 145
DB 150 LFYPOFLCEPDSPK 164

RESULT 13
US-09-987-675-5
Sequence 5, Application US/09987675
Patent No. US20020169282A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GRFN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,675
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/097,094
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-675-5

Query Match 27.6%; Score 264.5; DB 9; Length 118;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 45; Indels 5; Gaps 3;
QY 22 LLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDCYQELFDQGGHP 81
DB 2 LLDLKSMEIKVTGNALNTNFGYCYGCGWGGRTPKDGTDMCCWAHDHCYGRLEEGCNI 61
QY 82 YVDHYDHTIENNTIEVCSDLNKTCDKQTCMCKNMVLCMLN--QTYREYRGFLNVYC 138
DB 62 RTQSYKYRFAMGV-VTCEP--GPCHVNLACDRKLVCLKRLNLSYNPQYQYFPNLC 117

RESULT 14
US-09-987-655-5
Sequence 5, Application US/09987655
Patent No. US20020132975A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.

APPLICANT: Simon, Reyna
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GRFN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,655
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/097,094
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-655-5

Query Match 27.6%; Score 264.5; DB 10; Length 118;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 45; Indels 5; Gaps 3;
QY 22 LLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDCYQELFDQGGHP 81
DB 2 LLDLKSMEIKVTGNALNTNFGYCYGCGWGGRTPKDGTDMCCWAHDHCYGRLEEGCNI 61
QY 82 YVDHYDHTIENNTIEVCSDLNKTCDKQTCMCKNMVLCMLN--QTYREYRGFLNVYC 138
DB 62 RTQSYKYRFAMGV-VTCEP--GPCHVNLACDRKLVCLKRLNLSYNPQYQYFPNLC 117

RESULT 15
US-09-925-297-511
Sequence 511, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 511
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SITE
LOCATION: (156)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-511

Query Match 23.0%; Score 220.5; DB 10; Length 156;
Best Local Similarity 32.5%; Pred. No. 2.1e-13;
Matches 49; Conservative 23; Mismatches 60; Indels 19; Gaps 7;
QY 3 KFTTVAL---AGSVLSTANGSLNLKAMVEAV-TGRSAILSFVGYCYGCGLGGRGQPKD 58
DB 10 KLLVLAVLLTVAADSGISPRAVWQFRKMKVCIPGSDPFLFNNYGYCYGCGLGSGTPTVD 69
QY 59 EVDWCCHAHDCYQELFDQGGHPYVDHYDHTIENNTIEVCSDLNKTCDKQ 109
DB 70 ELDKCCQTHDNCYDQAKKLDCKFLD---NPYTHYTSYSC--SGSAITCSSKNK--ECEAF 124
QY 110 TCMCKNMVLCMLNQTYREYRGFLNVYCQ 139
DB 125 ICNCDRNAICFSKAPYNKAHNLDTKTYCQ 155

Mon Feb 10 11:36:15 2003

Search completed: February 10, 2003, 10:41:12
Job time : 13 secs

us-09-975-456b-2.rapb

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:31 ; Search time 17 Seconds
(without alignments)
950.034 Million cell updates/sec

Title: US-09-975-456b-2
Perfect score: 957
Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	309.5	32.3	138	JC1342	phospholipase A2
2	302.5	31.6	144	PSHUYF	phospholipase A2
3	298.5	31.2	122	PSVXF	phospholipase A2
4	297	31.0	145	I48093	phospholipase A2
5	294.5	30.8	146	A35493	phospholipase A2
6	287.5	30.0	146	A33394	phospholipase A2
7	281	29.4	146	I48342	phospholipase A2
8	280.5	29.3	138	S59522	phospholipase A2
9	279.5	29.2	137	S68429	phospholipase A2
10	278.5	29.1	122	PSABA	myotoxin precursor
11	278.5	29.1	138	I30098	phospholipase A2
12	277.5	28.0	146	JU0283	phospholipase A2
13	275.5	28.8	138	A49959	phospholipase A2
14	275	28.7	130	A54762	phospholipase A2
15	272.5	28.5	138	PSRSAT	phospholipase A2
16	272.5	28.5	138	PSVIAC	phospholipase A2
17	272.5	28.5	138	I51386	phospholipase A2
18	269.5	28.2	138	S10992	phospholipase A2
19	269	28.1	138	F48188	ammodytin L precursor
20	268.5	28.1	138	PSVIAA	phospholipase A2
21	267.5	28.0	138	I51380	phospholipase A2
22	267	27.9	158	B54762	phospholipase A2
23	264.5	27.6	121	PSNNAM	phospholipase A2
24	264	27.4	124	I51390	phospholipase A2
25	261.5	27.3	123	B53872	phospholipase A2
26	261.5	27.3	138	S10333	ammodytin B precursor
27	260	27.2	122	A33317	phospholipase A2
28	260	27.2	138	E48188	phospholipase A2
29	259.5	27.1	122	S09314	phospholipase A2

30	258.5	27.0	137	1	JC4877	phospholipase A2
31	258	27.0	138	2	D48188	phospholipase A2
32	254	26.5	122	2	S13900	phospholipase A2
33	251.5	26.3	122	2	A25805	phospholipase A2
34	251.5	26.3	138	1	PSRSBT	phospholipase A2
35	251.5	26.3	138	1	I51381	phospholipase A2
36	250.5	26.2	121	1	PC4024	phospholipase A2
37	250.5	26.2	122	2	S33287	phospholipase A2
38	250.5	26.2	144	2	JN0480	phospholipase A2
39	250	26.1	125	2	JX0052	phospholipase A2
40	249.5	26.0	138	2	JC5243	phospholipase A2
41	249	26.0	121	2	S17860	phospholipase A2
42	249	26.0	122	2	A53872	phospholipase A2
43	249	26.0	137	2	S22388	phospholipase A2
44	249	26.0	138	2	A48188	phospholipase A2
45	248.5	26.0	138	1	PSRSB2	phospholipase A2

ALIGNMENTS

RESULT 1

JC1342

phospholipase A2 (EC 3.1.1.4) precursor - halys viper

C:Species: Agkistrodon halys (halys viper)

C>Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998

C:Accession: JC1342

R:Pan, H.; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

Acta Biochim. Biophys. Sin. 28, 579-582, 1996

A:Title: Cloning of the BPUA2 gene from Agkistrodon halys Pallas.

A:Reference number: JC1342

A:Contents: Snake venom

A:Accession: JC1342

A:Molecule type: mRNA

A:Residues: 1-138 <PAN>

A:Note: the authors translated the codon GAC for residue 54 as Asn

C:Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond o

C:Superfamily: phospholipase A2

C:Keywords: carboxylic ester hydrolase

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-138/Product: phospholipase A2 #status predicted <WAT>

Query Match 32.3% Score 309.5; DB 2; Length 138;
Best Local Similarity 39.5%; Pred. No. 1.8e-19;
Matches 58; Conservative 26; Mismatches 52; Indels 11; Gaps 5;

QY 1 MKKFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYCYGLGGRGPKDEV 60
Db 1 MRALWIVAVL---LLGVGSLLOFRKMKMTGKEPVVSYAFYCYCGSGRGPDKDAT 56
QY 61 DMCCAHDCCYOELFDGCHPVVDHYDHTIENNTIIVCSDLNKTCDKOTCMCKNMVLC 120
Db 57 DRCCFVHDCYBKL--TGCDPKWDDTYTSWKNGT-IVCG--GDDPKCKKEVCECDKAAIC 111
QY 121 LMN--QTYREYRGFLNVCQGTPTNC 145
Db 112 FRDLNLTQKRYMTYPNLCSSKSEKC 138

RESULT 2

PSHUYF

phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human

N:Alternate names: phosphatidylcholine 2-acylhydrolase; placental PLA2; platelet-secr

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 15-Sep-2000

C:Accession: A32862; B32862; A60265; A32847; A60263; A31350; P70056; A32913; A60265;

R:Kramer, R.M.; Hesselton, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard,

J. Biol. Chem. 264, 5768-5775, 1989

A:Title: Structure and properties of a human non-pancreatic phospholipase A-2.

A:Reference number: A32862; MUID:89174633; PMID:2525633

A:Accession: A32862

A>Status: not compared with conceptual translation

A:Molecule type: DNA

Teater, C.; Warrick, M.W.; Jones, N.D.
submitted to the Brookhaven Protein Data Bank, May 1992
A:Reference number: A51043; PDB:1BBC
A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Go
Teater, C.; Warrick, M.W.; Jones, N.D.
Nature 352, 79-82, 1991
A:Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase A2
A:Reference number: A58514; MUID:91287826; PMID:2062381
A:Contents: annotation; X-ray crystallography
C:Genetics:
A:Gene: GDB:PLA2G2A; PLA2B; PLA2L
A:Cross-references: GDB:120296; OMIM:172411
A:Map position: 1p36.1-1p35
A:Introns: 14/1; 62/2; 98/1
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degra
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-144/Product: phospholipase A2 IIA #status experimental <MAT>
F:46-137,48-64,63-117,69-144,70-110,79-103,97-108/Disulfide bonds: #status experiment
F:47,49,51,68/Binding site: calcium (His, Gly, Asp) #status predicted
F:67,111/Active site: His, Asp #status predicted
Query Match 31.6%; Score 302.5; DB 1; Length 144;
Best Local Similarity 38.8%; Pred. No. 7.2e-19;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
QY 1 MKKEFTVAIAGSVLSTAGHSILNLKAMVEAVTGRSAIISFVGYCYGCGLGGRGPKDEV 60
DB 1 MKTLLLAIVMIFGLQAHGDLNLFHMRKILTTGKRAALSYGFYCHGCGVGRGSPKDAT 60
QY 61 DWCCAHDCYQELFDQCCHPYVDHYDHTIENNTIEVCSDLNTECDKOTCMDCDNNVLC 120
DB 61 DRCCVTHDCYKLEKRGCGTKFLSYKFS-NSGSRITCA--KQDSRCSQLCEDKAAATC 117
QY 121 LMNQ--TYREYRGLNLYCOGPTPNC 145
DB 118 FARNKTTYNKQYYSNKHCRGSGTPRC 144
RESULT 3
PSTVXF
phospholipase A2 (EC 3.1.1.4) X - habu
N:Alternate names: phosphatidylcholine 2-acylhydrolase
C:Species: Trimeresurus flavoviridis (habu)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
C:Accession: A25500
R:Kini, R.M.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A:Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
A:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metall
F:26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted
F:27,29,31,48/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F:47,89/Active site: His, Asp #status predicted
Query Match 31.2%; Score 298.5; DB 1; Length 122;
Best Local Similarity 41.3%; Pred. No. 1.4e-18;
Matches 52; Conservative 23; Mismatches 44; Indels 7; Gaps 4;
QY 22 LLNLKAMVEAVTGRSAIISFVGYCYGCGLGGRGPKDEVDMCCHADCCYQELFDQGGCHP 81
DB 22 LLNLKAMVEAVTGRSAIISFVGYCYGCGLGGRGPKDEVDMCCHADCCYQELFDQGGCHP 81

A:Residues: 1-144 <KRA>
A:Accession: B32862
A:Molecule type: protein
A:Residues: 21-39 <KR2>
A:Note: this protein was also detected in platelets
R:Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
Adv. Exp. Med. Biol. 275, 35-53, 1990
A:Title: Structure and properties of a secreted platelet phospholipase A-2 from human platelets
A:Reference number: A60266; MUID:91050834; PMID:2239446
A:Accession: A60266
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-144 <KR3>
R:Seilhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
J. Biol. Chem. 264, 5335-5336, 1989
A:Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
A:Reference number: A32847; MUID:89174566; PMID:2925608
A:Accession: A32847
A:Molecule type: mRNA
A:Residues: 1-144 <SEI>
A:Cross-references: GB:J04704; EMBL:M22430; NID:g190886; PIDN:AAA36550.1; PID:g190889
R:Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.
Adv. Exp. Med. Biol. 279, 173-184, 1990
A:Title: Isolation and characterization of cDNA clones from human placenta coding for ph
A:Reference number: A60263; MUID:91263879; PMID:1710870
A:Accession: A60263
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-144 <CRO>
R:Lai, C.Y.; Wada, K.
Biochem. Biophys. Res. Commun. 157, 488-493, 1988
A:Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
A:Reference number: A31350; MUID:89076274; PMID:3202859
A:Accession: A31350
A:Molecule type: protein
A:Residues: 21-33 <LAI>
R:Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
J. Biochem. 104, 326-328, 1988
A:Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
A:Reference number: PT0056; MUID:8917814; PMID:3240982
A:Accession: PT0056
A:Molecule type: protein
A:Residues: 21-46, 'X', 48-54 <HAR>
R:Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
Biochem. Biophys. Res. Commun. 163, 42-48, 1989
A:Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A:Reference number: A32913; MUID:89374261; PMID:2775276
A:Accession: A32913
A:Molecule type: protein
A:Residues: 21-144 <KAN>
R:Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A:Title: Purification and characterization of a phospholipase A-2 from human osteoarthr
A:Reference number: A60265; MUID:91050835; PMID:2146857
A:Accession: A60265
A:Molecule type: protein
A:Residues: 21-45, 'X' <PAR>
R:Recklies, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
A:Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix p
A:Reference number: A61201; MUID:92029121; PMID:1930329
A:Accession: A61201
A:Molecule type: protein
A:Residues: 21-40 <REC>
R:Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.
Inflammation 15, 355-366, 1991
A:Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock
A:Reference number: A61634; MUID:92098137; PMID:1757123
A:Accession: A61634
A:Molecule type: protein
A:Residues: 21-44 <GRE>
R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods

Db 2 LLOFRKMKWTKGKPIVAFVGCYCGKGRGKPKDTRCCFVHDDCCYEKV--TGCDP 59
 QY 82 YVDHYDHTTENNTIIVCSDLNTECDKQTCMCDKNWVLCMLN--QTYREYRGFLNVYQC 139
 Db 60 KWSYYSLENG-DIVCG--GDPYCTKVKCECDKAAICFRDNLKTYKNRYMTPDIFCT 116
 QY 140 GTPPNC 145
 Db 117 DPTEGC 122

RESULT 4

I48093
 phospholipase A2 (EC 3.1.1.4) type II - guinea pig
 C:Species: Cavita porcellus (guinea pig)
 C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999
 C:Accession: I48093
 R:Vial, D.; Senorato-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
 J. Biol. Chem. 270, 17327-17332, 1995
 A:Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulation of type-II phospholipase A2 in alveolar macrophages. Down-regulation of type-II phospholipase A2 in alveolar macrophages. Down-regulation of type-II phospholipase A2 in alveolar macrophages.
 A:Reference number: I48093; MUID:95340522; PMID:7615534
 A:Accession: I48093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-145 <RES>
 A:Cross-references: EMBL:X82631; NID:g951010; PIDN:CAA57953.1; PID:g951011
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase
 F:67,112/Active site: His, Asp #status predicted

Query Match 31.0%; Score 297; DB 2; Length 145;
 Best Local Similarity 37.4%; Pred. No. 2.1e-18;
 Matches 55; Conservative 23; Mismatches 65; Indels 4; Gaps 3;
 QY 1 MKKFTVATAGSVLSTAHGSLNLMKAMVEAVTGRSAILSFVGYCYGCGGGRGQPKDEV 60
 Db 1 MKLLLLLVVNASDLPQAHGHLKQFTTEMIKLTGKNGLTSGYAGYCGVGGGRTPKDAT 60
 QY 61 DWCHADCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNWVLC 120
 Db 61 DRCCVRHDCYDRLMKRGCGTKFLNYRFT-HKGSITCS-VKQNSCQKQCECDKAAAYC 118
 QY 121 LMN--QTYREYRGFLNVYCOGPTPNC 145
 Db 119 FAANKSYRRYQFYNGLCRGKTPSC 145

RESULT 5

A35493
 phospholipase A2 (EC 3.1.1.4) II precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 18-Jun-1999
 C:Accession: A35493; S11388; S71310
 R:Komada, M.; Kudo, I.; Inoue, K.
 Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990
 A:Title: Structure of gene coding for rat group II phospholipase A-2.
 A:Reference number: A35493; MUID:90267443; PMID:2346480
 A:Accession: A35493
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <KOM>
 A:Cross-references: GB:M37127; NID:9204318; PIDN:AAA41223.1; PID:g204319
 A:Note: the authors translated the codon TAT for residue 42 as Thr
 R:Kusunoki, C.; Sato, S.; Kobayashi, M.; Niwa, M.
 Biochim. Biophys. Acta 1087, 95-97, 1990
 A:Title: Structure of genomic DNA for rat platelet phospholipase A(2).
 A:Reference number: S11388; MUID:90381322; PMID:2400792
 A:Accession: S11388
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <KUS>
 A:Cross-references: EMBL:X51529; NID:g956930; PIDN:CAA35909.1; PID:g56931
 R:Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch

Arch. Biochem. Biophys. 331, 95-103, 1996
 A:Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from rat platelet phospholipase A2
 A:Reference number: S71310; MUID:96268465; PMID:8660688
 A:Accession: S71310
 A:Molecule type: protein
 A:Residues: 22-29, 'X', '31-32, 'X', '34 <AAR>
 A:Experimental source: kidney
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase; lipid degradation
 F:68,113/Active site: His, Asp #status predicted

Query Match 30.8%; Score 294.5; DB 2; Length 146;
 Best Local Similarity 42.3%; Pred. No. 3.5e-18;
 Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;

QY 7 VAILA-GSVLSTAHGSLNLMKAMVEAVTGRSAILSFVGYCYGCGGGRGQPKDEVWCCH 65
 Db 9 VVIMAFGSI--QVQGSLLLEFGQMLFKTKRADVSYGFGCHGCGVGGSPKDATDWCCV 66
 QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNWVLCMLN--N 123
 Db 67 THDCCYNRLKRGCGTKFLTYKFSYRGG-QISCS-TNQDSCKQLCCQCDKAAAEFCFARK 124
 QY 124 QTYREYRGFLNVYCOGPTPNC 145
 Db 125 KSYSLKYQFYLNKFCRGKTPSC 146

RESULT 6

A33394
 phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
 C:Accession: A33394; JU0131
 R:Ishizaki, J.; Ohara, O.; Nakamura, E.; Tanaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
 A:Title: cDNA cloning and sequence determination of rat membrane-associated phospholipase A2
 A:Reference number: A33394; MUID:89350908; PMID:2764915
 A:Accession: A33394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-146 <ISH>
 A:Cross-references: GB:M25148
 R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
 J. Biochem. 106, 545-547, 1989
 A:Title: Structure of cDNA coding for rat platelet phospholipase A2.
 A:Reference number: JU0131; MUID:90110043; PMID:2606907
 A:Accession: JU0131
 A:Molecule type: mRNA
 A:Residues: 1-146 <KOM>
 A:Cross-references: GB:D00523; NID:g220857; PIDN:BAA00410.1; PID:g220858
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-146/Product: phospholipase A2 #status predicted <MAT>
 F:68,113/Active site: His, Asp #status predicted

Query Match 30.0%; Score 287.5; DB 2; Length 146;
 Best Local Similarity 41.5%; Pred. No. 1.4e-17;
 Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;

QY 7 VAILA-GSVLSTAHGSLNLMKAMVEAVTGRSAILSFVGYCYGCGGGRGQPKDEVWCCH 65
 Db 9 VVIMAFGSI--QVQGSLLLEFGQMLFKTKRADVSYGFGCHGCGVGGSPKDATDWCCV 66
 QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNWVLCMLN--N 123
 Db 67 THDCCYNRLKRGCGTKFLTYKFSYRGG-QISCS-TNQDSCKQLCCQCDKAAAEFCFARK 124
 QY 124 QTYREYRGFLNVYCOGPTPNC 145
 Db 125 KSYSLKYQFYLNKFCRGKTPSC 146

A:Molecule type: mRNA
A:Residues: 1-138 <TSA>
A:Cross-references: EMBL:X77645
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:63.105/Active site: His, Asp #status predicted

Query Match 29.3%; Score 280.5; DB 2; Length 138;
Best Local Similarity 37.4%; Pred. No. 5.2e-17;
Matches 55; Conservative 29; Mismatches 52; Indels 11; Gaps 5;

QY 1 MKKFTTVAIIAGSVLSTAHGSLNLKAMVEAVTGRSAITLSFVGYCYGGLGGRGQPKDEV 60
DB 1 MRTLWIAVL-----LLGVEGNLLQFNKIKMTKKNALFFYSYSGYCGWGGQKPKDAT 56
QY 61 DWCHAHDCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVL 120
DB 57 DRCCFVHDCYCKGLTD--CSPKSDIYSYWKTI--IICGE--GTECEKKICECDRAAVC 111
QY 121 LMN--QTYREYRGFLNVYCOGPTPNC 145
DB 112 LGHNLRTYKKRYMFPDFLCTDPSEKC 138

RESULT 9

myotoxin precursor - southern copperhead
C:Species: Agkistrodon contortrix contortrix (southern copperhead)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: S68429; S74296
R:de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A:Title: cDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxi
A:Reference number: S68429; MUID:96154243; PMID:8579368
A:Accession: S68429

A:Molecule type: mRNA
A:Residues: 1-137 <DEA>
A:Cross-references: EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g809485
A:Accession: S74296
A:Molecule type: protein
A:Residues: 17-36 <DER>
C:Superfamily: phospholipase A2
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-137/Product: myotoxin #status experimental <MAT>

Query Match 29.2%; Score 279.5; DB 2; Length 137;
Best Local Similarity 39.9%; Pred. No. 6.3e-17;
Matches 57; Conservative 23; Mismatches 52; Indels 11; Gaps 5;

QY 1 MKKFTTVAIIAGSVLSTAHGSLNLKAMVEAVTGRSAITLSFVGYCYGGLGGRGQPKDEV 60
DB 1 MRTLWIAVL-----LVGVEGSLLELGRKILQETGKNATISYSGYCGWGGHGRGQPKDAT 56
QY 61 DWCHAHDCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVL 120
DB 57 DRCCFVHDCYCKGLTD--CNHKTDRYSYKNKA--IICEE--KNPCLKEMCECDKAVAIC 111
QY 121 LMN--QTYREYRGFLNVYCOGP 141
DB 112 LRENLDYTKRYKAYFKCKKP 134

RESULT 10

PSABA
phospholipase A2 (EC 3.1.1.4) - mamushi
N:Alternate names: phosphatidylcholine 2-acylhydrolase
C:Species: Agkistrodon blomhoffi (mamushi)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 26-Feb-1999
C:Accession: A00766; S43474
R:Forst, S.; Weiss, J.; Blackburn, P.; Frangione, B.; Goni, F.; Eisbach, P.
Biochemistry 25, 4309-4314, 1986
A:Title: Amino acid sequence of a basic Agkistrodon halys blomhoffii phospholipase A2
A:Reference number: A00766; MUID:87000546; PMID:3530322

RESULT 7
I48342
phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48342; PC2009; S35948; I49352
R:Mulherkar, R.; Rao, R.S.; Wagie, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A:Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: F
A:Reference number: I48342; MUID:94029955; PMID:8267767
A:Accession: I48342
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-146 <MUL2>
A:Cross-references: EMBL:X74266; NID:g557247; PIDN:CAA52325.1; PID:g557248
R:Mulherkar, R.; Rao, R.S.; Wagie, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993

A:Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: F
A:Reference number: PC2009; MUID:94071967; PMID:8250944
A:Accession: PC2009

A:Molecule type: mRNA
A:Residues: 22-146 <MUL2>
A:Note: correction of S35948
R:Mulherkar, R.; Rao, R.; Wagie, A.; Patki, V.; Deo, M.
submitted to the EMBL Data Library, July 1993
A:Reference number: S35948
A:Accession: S35948

A:Molecule type: mRNA
A:Residues: 22-115, 'R', 118-146 <MUL>
A:Cross-references: EMBL:X74266
R:Kennedy, B.P.; Payette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.-
J. Biol. Chem. 270, 22378-22385, 1995
A:Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred
A:Reference number: I49352; MUID:95403435; PMID:7673223
A:Accession: I49352

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A:Cross-references: EMBL:U32358; NID:g984836; PIDN:AAC52252.1; PID:g984837
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:68.113/Active site: His, Asp #status predicted

Query Match 29.4%; Score 281; DB 2; Length 146;
Best Local Similarity 37.1%; Pred. No. 5e-17; Mismatches 56; Indels 8; Gaps 4;
Matches 53; Conservative 26

QY 9 ILAGSVLSTA---HGSLNLKAMVEAVTGRSAITLSFVGYCYGGLGGRGQPKDEVWCC 64
DB 6 LLAASIMAFGSIQDQGNIAQFEMIRLTKRAELSYAFYGCGLGGKSPKDATDRCC 65
QY 65 HAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKOTCMCDKNMVLCLM-- 122
DB 66 VTHDCCYKSLKSGCGTKLLTYKSHOGG-QITCS-ANQNSCKRLQCQCDKAAAEAFARN 123
QY 123 NQTYREYRGFLNVYCOGPTPNC 145
DB 124 KKTYSLKTYQFPNMFCKGKPKC 146

RESULT 8

S59522
phospholipase A2 (EC 3.1.1.4) precursor - Chinese habu
C:Species: Trimeresurus mucrosquamatus (Chinese habu)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 07-May-1999
C:Accession: S59522
R:Tsal, I.H.; Lu, P.J.; Wang, Y.M.; Ho, C.L.; Liaw, L.L.
Biochem. J. 311, 895-900, 1995
A:Title: Molecular cloning and characterization of a neurotoxic phospholipase A(2) from
A:Reference number: S59522; MUID:96067607; PMID:7487947
A:Accession: S59522
A:Status: preliminary

A:Accession: A00766
A:Molecule type: protein
A:Residues: 1-122 <FOR>
R:Note: the identification of 74-Val is tentative
R:Dua, R.; Cho, W.
Eur. J. Biochem. 221, 481-490, 1994
A:Title: Inhibition of human secretory class II phospholipase A(2) by heparin.
A:Reference number: S43474; PMID:94222096; PMID:8168536
A:Accession: S43474
A:Molecule type: protein
A:Residues: 1-19;50-56 <DUA>
C:Complex: homodimer
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-2-acyl-sn-glycero-3-phosphate and a diacylglycerol.
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle.
C:Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metalloprotease; phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metalloprotease; phospholipase A2
F:4.64/Binding site: micellar substrate (Gln, Tyr) #status predicted
F:6.115,28-44, 43-95,50-88,57-81,75-86/Disulfide bonds: #status predicted
F:27,29,31,48/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F:47,89/Active site: His, Asp #status predicted
F:48-122/Disulfide bonds: #status experimental

[illegible]

b 117 SKSEKC 122
 :
 RESULT 11
 50098
 phospholipase a2 - jararacussu
 :Species: Bothrops jararacussu (jararacussu)
 :Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
 :Accession: I50098; S44247
 :Moura-da-Silva, A.M.; Palme, M.J.; Diniz, M.R.; Theakston, R.D.; Crampton, J.M.
 :Mol. Evol. 41, 174-179, 1995
 :Title: The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake venom
 :Reference number: I50098; MUID:9535872; PMID:7666446
 :Accession: I50098
 :Status: preliminary; translated from GB/EMBL/DBJ
 :Molecule type: mRNA
 :Residues: 1-138 <MOU>
 :Cross-references: EMBL:X76289; NID:g475923; PIDN:CAAS3921.1; PID:g475924
 :Genetics:
 :Gene: PLA-2
 :Superfamily: phospholipase A2
 :63.105/Active site: His, Asp #status predicted

```

Query Match      29.1%; Score 278.5; DB 2; Length 138;
Best Local Similarity 37.4%; Pred. No. 7.8e-17;
Matches 55; Conservative 21; Mismatches 60; Indels 11; Gaps 5;

1 MKKFTTVAIIAGSVLSTAHGSLNLNKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEV 60
  | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
1 MRTLWIMAVL-----LVGVEDGLWQFGOMILKETGLPPRYTTYTCYCGYGGWQQQPKDAT 56
  | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

61 DWCCHAHDCCYQBLEDOGHCPHYVDHTIENNTIVCSDLNKTCEDKQTCMCDKNMVLVC 120
  | | | | | | | | | | | | | | | | : | : | : | : | : | : | : | : |
57 DRCCFVHDCCYCKL--TNCKPKTDRISYRENGV-IICGE--GTPCEKQICECDKAAAVC 111
  | | | | | | | | | | | | | | | | : | : | : | : | : | : | : | : |

121 LMN--QTYREYRGFLNNVYCGQPTPNC 145

```

```

Db      112  FRENLETKRYMAYDPDVLCKPAEKC 138
:||||:| :|||:| :|||:|
RESULT 12
JU0283
Phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07
C:Accession: JU0283
R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A:Title: Structure of cDNA coding for rat platelet phospholipase A2.
A:Reference number: JU0131; MUID:90110043; PMID:2606907
A:Accession: JU0283
A:Molecule type: mRNA
A:Residues: 1-146 <KOW>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:1-21/domain: signal sequence #status predicted <SIG>
F:22-146/product: phospholipase A2 #status predicted <MAG>
F:68,113/Active site: His, Asp #status predicted

```

Query Match	29.0%;	Score	277.5;	DB 2;	Length	146;			
Best Local Similarity	40.8%;	Pred.	No. 1e-16;						
Matches	58;	Conservative	20;	Mismatches	57;	Indels	7;	Gaps	5;
QY	7	VALLA-GSVLSTANGSLINLAKMVAEVTGRSAILSFVGYGCGGLGQPKRDEVDWCH	65						
Ddb	9	VWIAFGSII--QVGSLSLEFGQILFKTKRADVSYGFGYCHGVGGRSPKDATDWCV	66						
QY	66	AHDCCYQELFDQGHCPYVDHYDHTIENNTFVCSDLNKTCEDKQTCMCDKNVLCM--N	123						
Ddb	67	THGCCYNLLEKRCGGCTFLYIKFSYRGG--QISCS-TNQDSCKRQLQCQCDKAAAECFARNK	124						
QY	124	QTYREERYGFLNVYCGGPTNC	145						
Ddb	125	KSYLKYQFYPNKFCRKGKTPSC	146						

```

RESULT 13
A449959
:Phospholipase A2 (EC 3.1.1.4) low molecular weight, precursor - human
::Species: Homo sapiens (man)
::Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
::Accession: A49959
:Chen, J.; Chen, J.; Engle, S.J.; Seilhamer, J.J.; Tischfield, J.A.
:J. Biol. Chem. 269, 2365-2368, 1994
::Title: Cloning and recombinant expression of a novel human low molecular weight Ca(
::Reference number: A49959; MUID: 94131989; PMID: 8300559
::Accession: A49959
::Status: preliminary
::Molecule type: mRNA
::Residues: 1-138 <CHE>
::Cross references: GB:U03090; NID:9460914; PIDN:AAC28886.1; PID:g460915
::Superfamily: phospholipase A2
::Keywords: carboxylic ester hydrolase
::67,111/Active site: His, Asp #status predicted

```

[illegible]

Search completed: February 10, 2003, 10:37:54
Job time : 18 secs

100

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:27 ; Search time 12 Seconds
(without alignments)
580.669 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	957	100.0	168	1 PA2F_HUMAN	Q9bzm2 homo sapien
2	747	78.1	168	1 PA2F_MOUSE	Q9qzt4 mus musculus
3	353	36.9	145	1 PA2D_HUMAN	Q9unk4 homo sapien
4	344.5	36.0	144	1 PA2D_MOUSE	Q9wvf6 mus musculus
5	319.5	33.4	138	1 PA2X_TRIFL	Q02517 trimeresuru
6	313.5	32.8	142	1 PA2E_MOUSE	Q9qul3 mus musculus
7	309	32.3	142	1 PA2E_HUMAN	Q9nzk7 homo sapien
8	302.5	31.6	144	1 PA2A_HUMAN	P06860 trimeresuru
9	298.5	31.2	122	1 PA2X_TRIFL	P47711 cavia porce
10	297	31.0	145	1 PA2M_CAVPO	Q9qxx3 mus musculus
11	287.5	30.0	146	1 PA2A_RAT	P4423 rattus norv
12	283.5	29.6	151	1 PA2X_MOUSE	P48076 mus musculus
13	282	29.5	150	1 PA2X_MOUSE	Q9qzt3 rattus norv
14	282	29.5	151	1 PA2X_RAT	P31482 mus musculus
15	281	29.4	146	1 PA2A_MOUSE	P97391 mus musculus
16	280.5	29.3	137	1 PA2M_MOUSE	P49121 agkistrodon
17	279.5	29.2	137	1 PA2M_AGKCL	P04417 agkistrodon
18	278.5	29.1	122	1 PA2L_AGKHA	P45881 bothrops ja
19	278.5	29.1	138	1 PA2L_BOTPI	P39877 homo sapien
20	275.5	28.8	138	1 PA2S_HUMAN	P08878 crotalus du
21	272.5	28.5	138	1 PA2A_CRODU	P11407 vipera ammo
22	272.5	28.5	138	1 PA2C_VIPAA	Q9pve3 bothrops as
23	272	28.4	138	1 PA2B_BOTAS	P70088 trimeresuru
24	272	28.4	138	1 PA26_TRIGA	P48650 echis carin
25	269.5	28.2	122	1 PA2N_ECHCA	P51433 rattus norv
26	268.5	28.1	137	1 PA2S_RAT	P00626 vipera ammo
27	268.5	28.1	138	1 PA2A_VIPAA	O15496 homo sapien
28	268.5	28.1	155	1 PA2X_HUMAN	P17935 vipera ammo
29	267.5	28.0	138	1 PA2L_VIPAA	P39878 rattus norv
30	267	27.9	150	1 PA2C_RAT	P04361 agkistrodon
31	264.5	27.6	121	1 PA2H_AGKPI	Q91834 bothrops mo
32	262	27.4	122	1 PA2B_BOTMO	P51972 agkistrodon
33	261.5	27.3	123	1 PA21_AGKPI	

34	261.5	27.3	138	1 PA2B_VIPAA	P14424 vipera ammo
35	260	27.2	122	1 PA22_AGKHA	P20249 agkistrodon
36	259.5	27.1	122	1 PA21_BOTAS	P20474 bothrops as
37	258	27.0	138	1 PA2B_TRIFL	P20381 trimeresuru
38	257.5	26.9	121	1 PA22_BOTAS	P24605 bothrops as
39	256.5	26.8	121	1 PA22_BOTPI	P82287 bothrops pi
40	255.5	26.7	138	1 PA21_TRIGA	P20476 trimeresuru
41	252.5	26.4	121	1 PA21_BOTPI	P58399 bothrops pi
42	251.5	26.3	138	1 PA2B_CRODU	P07517 crotalus du
43	250.5	26.2	121	1 PA2H_BOTPI	Q90249 bothrops ja
44	250.5	26.2	122	1 PA2B_VIPBB	P31854 vipera beru
45	249.5	26.1	138	1 PA2A_VIPBA	Q98996 vipera pala

ALIGNMENTS

RESULT 1

PA2F_HUMAN

ID PA2F_HUMAN STANDARD; PRT; 168 AA.
AC Q9BZM2; Q9H506;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Group IIF secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylglycerolase GIIF) (GIIF SPLA2) (SPLA(2)-IIF).
GN PLA2G2F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=20563827; PubMed=11112443;
RA Valentin E., Singer A.G., Ghomashchi F., Lazdunski M., Gelb M.H.,
RA Lambeau G.;
RT "Cloning and recombinant expression of human group IIF-secreted
phospholipase A(2).";
RL Biochem. Biophys. Res. Commun. 279:223-228(2000).
RN [2]
RP SEQUENCE OF 1-98 FROM N.A.

RA Wallis J.;
RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Hydrolyzes phosphatidylglycerol versus phosphatidylcholine with a 15-fold preference.
CC -I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -I- COFACTOR: Binds 1 calcium ion per subunit.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed at high levels in placenta, testis, thymus and at lower levels in heart, kidney, liver and prostate.
CC -I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
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CC -----
DR EMBL; AF306566; AAC50242.1; -
DR EMBL; AL158172; CAC13160.1; ALT_INIT.
DR HSSP; P82287; IQLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2
DR ProDom; PD000303; PhospholipaseA2
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.

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EMBL; AF166099; AAF04500.2; -.
HSSP; P00593; 4BP2.
MGM; MGI:1349661; Pla2g2f.
InterPro; IPR001211; PhospholipaseA2.
PRINTS; PR00389; PHPLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium.
SIGNAL 1 20 POTENTIAL.
CHAIN 21 168
T ACT_SITE 67 67 BY SIMILARITY.
T ACT_SITE 114 114 BY SIMILARITY.
T DISULFID 46 138 BY SIMILARITY.
T DISULFID 48 64 BY SIMILARITY.
T DISULFID 63 120 BY SIMILARITY.
T DISULFID 69 145 BY SIMILARITY.
T DISULFID 70 113 BY SIMILARITY.
T DISULFID 79 106 BY SIMILARITY.
T DISULFID 98 111 BY SIMILARITY.
T CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
T CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
T CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
T CA_BIND 51 51 VIA CARBONYL OXYGEN (BY SIMILARITY).
T CA_BIND 68 68 BY SIMILARITY.
SEQUENCE 168 AA; 18880 MW; 9E15FB6AC0F5450C CRC64;

Query Match 78.1%; Score 747; DB 1; Length 168;
Best Local Similarity 75.2%; Pred. No. 2.8e-60;
Matches 124; Conservative 20; Mismatches 21; Indels 0; Gaps 0

QY 1 MKKFTVAIALAGSVLSTAHGSLNLKAWBEAVTVGRSAILSFVGYGCYGLGGRGQPKDEV 60
||||| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 MKKFPAIATLAGSVVTAAHSLLNLSKVVEAITHRNSILSFVGYGCYGLGGRGHPMDEV 60
||||| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY 61 DWCHAHCCCYQLFDQCCHPYVDHYDHTENNNTIIVCSDLNKTECDKQFCMCDDKNVLVC 120
||||| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 61 DWCHAHCCCYEKLFQCGRYPVDHYDHRIENGTHWICTELNETCDKQTCDCDKSLTLC 120
||||| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY 121 LMNQTYREYRGFLNVYCQGTPNCISYEPPPEEVTCSSHOSAPP 165
| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 121 LKDHYRNKYRGYFNVCYGTPNCISYDPYPEEVTCGHGLPATP 165
| :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 3
ID PA2D_HUMAN STANDARD; PRT; 145 AA.

AC Q9UNK4; Q9UK01;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acetylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN PLA2GD OR SPLASH
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
RX MEDLINE=99386983; PubMed=10455175;
RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,

Best Local Similarity 45.1%; Pred. No. 3e-24; Matches 65; Conservative 20; Mismatches 52; Indels 7; Gaps 4;

QY 7 VAILAGSVL---STAHGSLNKLKAVEAVTGRSALTSFVGVCYGLGGGQPKDEVDWC 63
 DB 3 LALLGCLLAGITATATOGGLNKLKRWTHMTGKKAFFSWPVCCHGGLGGGQPKDWDWC 62
 QY 64 CHAHDCYCELFDOGHCPVVDHYDHTIENTEIVGSDLNKTECDKQTCMDKNVILCLMN 123
 DB 63 CQKHCCYAHKLKIDGCKSLTDNYSISQGT-IQCSN-NGSWCERQLCADCDEKVALCLKQ 120
 QY 124 --QTYREYRGFLNYVCQGPPTNC 145
 DB 121 NLDYNNKRLRYWPRCKGKTPAC 144

RESULT 5
 PA2Y_TRIFL STANDARD; PRT; 138 AA.
 ID PA2Y_TRIFL
 AC Q02517;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phospholipase A2 isozyme PL-X' precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92409555; PubMed=1528861;
 RA Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,
 RA Kihara H., Ohno M.;
 RT "Unusually high conservation of untranslated sequences in cDNAs for
 RT Trimeresurus flavoviridis phospholipase A2 isoforms.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).
 CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOLIPASES.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 CC
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 CC
 CC EMBL; D10721; BAA01564.1;
 CC HSSP; P51972; IVAP.
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1.
 CC PRINTS; PR00389; PHPLIPASEA2.
 CC ProDom; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2C; 1.
 CC PROSITE; PS00118; PA2_HIS; 1.
 CC PROSITE; PS00119; PA2_ASP; 1.
 CC Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom;
 CC Signal.
 CC
 CC FT CHAIN 1 16 PHOSPHOLIPASE A2 ISOZYME PL-X'.
 CC FT CHAIN 17 138 BY SIMILARITY.
 CC FT ACT_SITE 63 63 BY SIMILARITY.
 CC FT ACT_SITE 105 105 BY SIMILARITY.
 CC FT DISULFID 42 131 BY SIMILARITY.
 CC FT DISULFID 44 60 BY SIMILARITY.
 CC FT DISULFID 59 111 BY SIMILARITY.
 CC FT DISULFID 65 138 BY SIMILARITY.

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustineich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombærts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RA Nature 409:685-690(2001).
 RL -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-
 CC linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed
 CC than the other phospholipids examined.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic
 CC (isoform 2) (Potential).
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Expressed in several tissues including
 CC pancreas, spleen, thymus, skin, lung, and ovary.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 CC
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 CC
 CC EMBL; AF112983; AAD51391.1;
 CC EMBL; AF124374; AAD42773.1;
 CC EMBL; AF188624; AAF09019.1;
 CC EMBL; AF169407; AAF42987.1;
 CC EMBL; AF169408; AAF42988.1;
 CC EMBL; AK018005; BAB31033.1;
 CC EMBL; AK004232; BAB23230.1;
 CC HSSP; P24605; 1CLP.
 CC MGD; MGT1341796; Pla2a2d.
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1.
 CC PRINTS; PR00389; PHPLIPASEA2.
 CC ProDom; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2C; 1.
 CC PROSITE; PS00119; PA2_HIS; 1.
 CC PROSITE; PS00118; PA2_ASP; 1.
 CC Hydrolyase; Lipid degradation; Signal; Calcium; Alternative splicing.
 CC POTENTIAL.
 CC SIGNAL 1 19
 CC CHAIN 20 144 GROUP IID SECRETORY PHOSPHOLIPASE A2.
 CC FT ACT_SITE 66 66 BY SIMILARITY.
 CC FT ACT_SITE 111 111 BY SIMILARITY.
 CC FT DISULFID 45 137 BY SIMILARITY.
 CC FT DISULFID 47 63 BY SIMILARITY.
 CC FT DISULFID 62 117 BY SIMILARITY.
 CC FT DISULFID 68 144 BY SIMILARITY.
 CC FT DISULFID 69 110 BY SIMILARITY.
 CC FT DISULFID 78 103 BY SIMILARITY.
 CC FT DISULFID 96 108 BY SIMILARITY.
 CC FT CARBOHYD 99 99 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CA_BIND 46 46 VIA CARBONYL OXYGEN (BY SIMILARITY).
 CC CA_BIND 48 48 VIA CARBONYL OXYGEN (BY SIMILARITY).
 CC CA_BIND 50 50 VIA CARBONYL OXYGEN (BY SIMILARITY).
 CC CA_BIND 67 67 BY SIMILARITY.
 CC FT VARSPLIC 1 26 MISSING (IN ISOFORM 2).
 CC SEQUENCE 144 AA; 16164 MW; 7697ADA07F8D270A CRC64;
 CC
 CC Query Match 36.0%; Score 344.5; DB 1; Length 144;

FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT CA_BIND 43 43 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 64 64 BY SIMILARITY.
 SQ SEQUENCE 138 AA; 15733 MW; 471B01878CCA1EDI CRC64;

 Query Match 33.4%; Score 319.5; DB 1; Length 138;
 Best Local Similarity 40.1%; Pred. No. 5e-22;
 Matches 59; Conservative 28; Mismatches 49; Indels 11; Gaps 5;

 QY 1 MKKFTVAILAGSVLSTAGHSLNLANKAVEAVTGRSAILSVGVGCGGLGGRGQPKDEV 60
 Db 1 MRTLIMAVL-----LVGVEGHLLOPRKMKKMTGKEIVSYAFVCGVCGGGRGPKDAT 56

 QY 61 DWCHAHDCCYBELFDQCHPYVDHYDHTIENNTVCSDLNKTECDKQTCMDCKNMVLC 120
 Db 57 DRCCFVHDCCEKV--TCDDPRWDYTYSSENG-DIVCGGDN--PCTKEVCECDKAAAI 111

 QY 121 LMN--OTYREYRGFLNVYCOGTPNC 145
 Db 112 FRDLNLTYYKRYMTFPDFICTDPTK 138

 RESULT 6
 ID PAZE_MOUSE STANDARD; PRT; 142 AA.
 AC Q90L3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).
 GN PLA2G2E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=2002639; PubMed=10531313;
 RA Valentini E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
 RT "On the diversity of secreted phospholipases A2. Cloning, tissue
 RT distribution, and functional expression of two novel mouse group II
 RT enzymes.";
 RL J. Biol. Chem. 274:31195-31202(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=BALB/C;
 RX MEDLINE=20148788; PubMed=10681567;
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
 RA Fujii N., Kawamoto K., Hanasaki K.;
 RT "Structures, enzymatic properties, and expression of novel human and
 RT mouse secretory phospholipase A(2)s.";
 RL J. Biol. Chem. 275:5785-5793(2000).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower
 CC levels in various other tissues.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF166098; AAF04499.1; -;
 DR EMBL: AF112984; AAF22290.1; -;
 DR HSSP: P14555; IPOD.
 DR MGD: MGI:1349660; Pla2g2e.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF00068; phoslip; 1
 DR PRINTS: PR00389; PHPLIPASEA2.
 DR ProDom: PD00303; PhospholipaseA2; 1.
 DR SMART: SM00085; PA2c; 1.
 DR PROSITE: PS00119; PA2_ASP; FALSE_NEG.
 DR PROSITE: PS00118; PA2_HIS; 1.
 KW Hydrolase; Lipid degradation; Signal; Calcium.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
 FT ACT_SITE 65 65 BY SIMILARITY.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT DISULFID 44 135 BY SIMILARITY.
 FT DISULFID 46 62 BY SIMILARITY.
 FT DISULFID 61 115 BY SIMILARITY.
 FT DISULFID 67 142 BY SIMILARITY.
 FT DISULFID 68 108 BY SIMILARITY.
 FT DISULFID 77 101 BY SIMILARITY.
 FT DISULFID 95 106 BY SIMILARITY.
 FT CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 66 66 BY SIMILARITY.
 SQ SEQUENCE 142 AA; 15942 MW; 8B0E3CC710A1F946 CRC64;

 Query Match 32.8%; Score 313.5; DB 1; Length 142;
 Best Local Similarity 42.2%; Pred. No. 1.8e-21;
 Matches 62; Conservative 20; Mismatches 58; Indels 7; Gaps 5;

 QY 1 MKKFTVAILAGSVLSTAGHSLNLANKAVEAVTGRSAILSVGVGCGGLGGRGQPKDEV 60
 Db 1 MKPPIALACLC-LVPLAGNLGVFGVMIERMTGKFA-LQYNDYGCYCGVGGSHWPVDET 58

 QY 61 DWCHAHDCCYBELFDQCHPYVDHYDHTIENNTVCSDLNKTECDKQTCMDCKNMVLC 120
 Db 59 DWCHAHDCCYGRLEKLGCDPKLEKYLFSITRD-NIFCA--GRTACQRTCEDKRAALC 115

 QY 121 LMN--OTYREYRGFLNVYCOGTPNC 145
 Db 116 FRNLNLTYYKRYAHYPNKLCCTGTPTPC 142

RESULT 7
 ID PAZE_HUMAN STANDARD; PRT; 142 AA.
 AC Q9NZK7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).
 GN PLA2G2E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20148788; PubMed=10681567;
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
 RA Fujii N., Kawamoto K., Hanasaki K.;
 RT "Structures, enzymatic properties, and expression of novel human and
 RT mouse secretory phospholipase A(2)s.";
 RL J. Biol. Chem. 275:5785-5793(2000).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Has a preference for
 CC arachidonic-containing phospholipids.

Mon Feb 10 11:36:18 2003

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CC -|- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O - 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -|- COFACTOR: Binds 1 calcium ion per subunit.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and
CC placenta.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC
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CC
CC EMBL; AF189279; AAF36541.1; -.
CC HSP; P14555; IPOD.
CC InterPro: IPR001211; PhospholipaseA2.
CC Pfam: PF000568; phoslip; 1.
CC PRINTS; PR00389; PHPLIPASEA2.
CC PRODOM; PD000303; PhospholipaseA2; 1.
CC SMART; SM00085; PA2c; 1.
CC PROSITE; PS00119; PA2_ASP; FALSE_NEG.
CC PROSITE; PS00118; PA2_HIS; 1.
CC Hydrolase; Lipid degradation; Signal; Calcium.
CC SIGNAL
CC CHAIN 1 19 POTENTIAL.
CC 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
CC ACT_SITE 65 65 BY SIMILARITY.
CC ACT_SITE 109 109 BY SIMILARITY.
CC DISULFID 44 135 BY SIMILARITY.
CC DISULFID 46 62 BY SIMILARITY.
CC DISULFID 61 115 BY SIMILARITY.
CC DISULFID 67 142 BY SIMILARITY.
CC DISULFID 68 108 BY SIMILARITY.
CC DISULFID 77 101 BY SIMILARITY.
CC DISULFID 95 106 BY SIMILARITY.
CC CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC CA_BIND 66 66 BY SIMILARITY.
CC SEQUENCE 142 AA; 15989 MW; 3C360EA710E141FB CRC64;
CC
CC Query Match 32.3%; Score 309; DB 1; Length 142;
CC Best Local Similarity 43.8%; Pred. No. 4.5e-21;
CC Matches 56; Conservative 18; Mismatches 48; Indels 6; Gaps 4;
CC
CC QY 20 GSLNLKAMVEAVTGRSAILSPVGYGCGYGLGGGQPKDEVDCCHAHDCYQELFDGCG 79
CC |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
CC Db 19 GNLVQGVMIKMTCKSA-LOYNDYGCYGGSHWPVDQTDWCCAHDCYGRLEKLCG 77
CC
CC QY 80 HPVVDHYDHTIENNTIVCSDLNTECDKOTCMCDKNVCLMNO--TYREYRGFLNVY 137
CC |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
CC Db 78 EPKLEKLYFSV-SERGIFCA--GRITTCQRLTCECDKRAALCFRRNLGTYNKRKYAHYFNKL 134
CC
CC QY 138 CQGPTEPC 145
CC |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
CC Db 135 CTGTPPC 142
CC
CC RESULT 8
CC PA2A_HUMAN STANDARD; PRT; 144 AA.
CC ID PA2A_HUMAN
CC AC P14555; Q9UCD2;
CC DT 01-JAN-1990 (Rel. 13, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
CC DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
CC DE (GTIC SPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).
CC GN PLA2G2A OR PLA2B OR RASF-A OR PLA2L.
CC OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE=Rheumatoid arthritic synovial fluid;
RX MEDLINE=89174566; PubMed=2925608;
RA Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
RA Kloss J., Johnson L.K.;
RA "Cloning and recombinant expression of phospholipase A2 present in
RT rheumatoid arthritic synovial fluid.";
RL J. Biol. Chem. 264:5335-5338(1989).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=89174633; PubMed=2925633;
RX Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
RA Tizard R., Pepinsky R.B.;
RA "Structure and properties of a human non-pancreatic phospholipase
RT A2.";
RT J. Biol. Chem. 264:5768-5775(1989).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=91050834; PubMed=2239446;
RX Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
RA "Structure and properties of a secreted phospholipase A2 from human
RT platelets.";
RL Adv. Exp. Med. Biol. 275:35-53(1990).
RN [4]
RN SEQUENCE FROM N.A.
RT TISSUE-Prostate;
RC Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 21-144.
RN TISSUE-Spleen;
RX MEDLINE=89374261; PubMed=2775276;
RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
RT "The primary structure of a membrane-associated phospholipase A2 from
RT human spleen.";
RL Biochem. Biophys. Res. Commun. 163:42-48(1989).
RN [6]
RN SEQUENCE OF 21-54.
RN TISSUE-Synovial fluid;
RX MEDLINE=89197814; PubMed=3240982;
RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
RT "Amino acid composition and NH2-terminal amino acid sequence of human
RT phospholipase A2 purified from rheumatoid synovial fluid.";
RL J. Biochem. 104:326-328(1988).
RN [7]
RN SEQUENCE OF 21-33.
RN TISSUE-Synovial fluid;
RC MEDLINE=89076274; PubMed=3202859;
RX Lai C.Y., Wada K.;
RA "Phospholipase A2 from human synovial fluid: purification and
RT structural homology to the placental enzyme.";
RL Biochem. Biophys. Res. Commun. 157:488-493(1988).
RN [8]
RN SEQUENCE OF 21-75.
RN TISSUE=Ileal mucosa;
RX MEDLINE=94002200; PubMed=8399335;
RX Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
RA "Purification and characterization of a phospholipase A2 from human
RT ileal mucosa.";
RT Biochim. Biophys. Acta 1170:125-130(1993).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287826; PubMed=2062381;
RX Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
RA Warrick M.W., Jones N.D.;
RT "Structure of recombinant human rheumatoid arthritic synovial fluid
RT phospholipase A2 at 2.2-A resolution.";
RT Nature 352:79-82(1991).

```


RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE=92054586; PubMed=1948070;
 RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
 RT Sigler P.B.;
 RT "Structures of free and inhibited human secretory phospholipase A2
 RL from inflammatory exudate.";
 RL Science 254:1007-1010(1991).
 [11]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE=95393225; PubMed=7664108;
 RA Schevitz R.W., Bach N.J., Carlson D.G., Chirgatz N.V., Clawson D.K.,
 RA Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
 RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
 RT "Structure-based design of the first potent and selective inhibitor
 RL of human non-pancreatic secretory phospholipase A2.";
 RL Nat. Struct. Biol. 2:458-465(1995).
 [12]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE=98207049; PubMed=9538252;
 RA Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;
 RT "Crystal structure of human secretory phospholipase A2-IIA complex
 RL with the potent indolizine inhibitor 120-1032.";
 RL J. Biochem. 123:619-623(1998).
 CC -!- FUNCTION: THOUGHT TO PARTICIPATE IN THE REGULATION OF THE
 CC PHOSPHOLIPID METABOLISM IN BIOMEMBRANES INCLUDING EICOSANOID
 CC BIOSYNTHESIS. CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-
 CC ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- MISCELLANEOUS: GROUP II PHOSPHOLIPASE A2 IS FOUND IN MANY CELLS
 CC AND ALSO EXTRACELLULARLY. THE MEMBRANE-BOUND AND SECRETED FORMS
 CC ARE IDENTICAL AND ARE ENCODED BY A SINGLE GENE.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M22430; AAA36550.1;
 DR EMBL: M22431; AAA36549.1;
 DR EMBL: BC005919; AAH05919.1;
 DR PIR: A32862; PSHUYF.
 DR PIR: A60266; A60266.
 DR PDB: 1AYP; 31-JUL-95.
 DR PDB: 1BBC; 31-OCT-93.
 DR PDB: 1POD; 31-OCT-93.
 DR PDB: 1POE; 31-OCT-93.
 DR PDB: 1KVO; 07-JUL-97.
 DR PDB: 1DB4; 12-NOV-99.
 DR PDB: 1DB5; 12-NOV-99.
 DR PDB: 1DCY; 12-NOV-99.
 DR Genew: HGNC:9031; PLA2G2A.
 DR MIM: 172411;
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF00068; Phoslip; 2.
 DR PRINTS: PR00389; PHPLIPASEA2.
 DR ProDom: PD000303; PhospholipaseA2; 1.
 DR SMART: SM00085; PA2C; 1.
 DR PROSITE: PS00118; PA2_HIS; 1.
 DR PROSITE: PS00119; PA2_ASP; 1.
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
 3D-structure.
 FT SIGNAL 1 20
 FT CHAIN 21 144
 FT ACT_SITE 67 67
 FT ACT_SITE 111 111
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 46 137
 FT DISULFID 48 64
 FT DISULFID 63 117
 FT DISULFID 69 144
 FT DISULFID 70 110
 FT DISULFID 79 103
 FT DISULFID 97 108
 FT CA_BIND 47 47
 FT CA_BIND 49 49
 FT CA_BIND 51 51
 FT CA_BIND 68 68
 FT CA_BIND 72 33
 FT HELIX 22 33
 FT HELIX 37 40
 FT TURN 41 41
 FT TURN 45 47
 FT HELIX 59 75
 FT TURN 76 78
 FT STRAND 88 91
 FT TURN 92 93
 FT STRAND 94 97
 FT HELIX 102 120
 FT TURN 121 121
 FT HELIX 122 124
 FT TURN 127 128
 FT TURN 130 131
 FT TURN 134 135
 SQ SEQUENCE 144 AA; 16083 MW; 923C5FA0C6979CDA CRC64;
 Query Match 31.6%; Score 302.5; DB 1; Length 144;
 Best Local Similarity 38.8%; Pred. No. 1.7e-20;
 Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
 Qy 1 MKKEFTVAIIAGSVLSTAHGSLNLKAMVEAVTGRSAIISFVGYCYGLGGRGQPRDEV 60
 Db 1 MKTLLAVIMFGLQAHGNLNFHFMKLTGKKAALSTGFGCHGVGGGRGSPRDT 60
 Qy 61 DMCCHADCCYQELFDGCHPYVDHDTHTENNTTEIVCSDLNKTCDKQTCMDKNMVL 120
 Db 61 DRCCVTHDCCYKRLKRGCCCTKFLSKFS-NSGSRITCA--KODSCRSQLCEDKAAAVC 117
 Qy 121 LMNO--TYREYRGFLNVYCGQPTPNC 145
 Db 118 FARKNTYKQYVYSNKHCRGSTPRC 144
 RESULT 9
 PA2X_TRIFL
 ID PA2X_TRIFL STANDARD; PRT; 122 AA.
 AC P06860;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phospholipase A2 isozyme PL-X (EC 3.1.1.4) (Phosphatidylcholine 2-
 DE acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87179112; PubMed=3564060;
 RA Kiri R.M., Kawabata S.-I., Iwanaga S.;
 RT "Comparison of amino terminal region of three isoenzymes of
 RT phospholipases A2 (TFV PL-Ia, TFV PL-IIb, TFV PL-X) from Trimeresurus
 RT flavoviridis (habu snake) venom and the complete amino acid sequence
 RT of the basic phospholipase, TFV PL-X.";
 RL Toxicon 24:1117-1129(1986).
 CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.

100

CC	EMBL; AF166097; AAF04498.2; -.
DR	EMBL; AF210429; AAG43522.1; -.
DR	HSSP; PG0593; 4BP2.
DR	MGD; MGI:1347522; Pla2g10.
DR	InterPro; IPR001211; PhospholipaseA2.
DR	Pfam; PF00068; phoslip; 1.
DR	PRINTS; PR00389; PHPELIPASEA2.
DR	ProDom; PD000303; PhospholipaseA2; 1.
DR	SMART; SM00085; PA2C; 1..
DR	PROSITE; PS00119; PA2_ASP; 1.
DR	PROSITE; PS00118; PA2_HIS; 1.
KW	Hydrolase; Lipid degradation; Calcium; Signal.
FT	SIGNAL 1 17
FT	PROPEP 18 28
FT	CHAIN 29 151
FT	ACT_SITE 74 74
FT	ACT_SITE 119 119
FT	DISULFID 39 97
FT	DISULFID 53 143
FT	DISULFID 55 171
GROUP X SECRETORY PHOSPHOLIPASE A2. BY SIMILARITY. BY SIMILARITY. POTENTIAL BY SIMILARITY. BY SIMILARITY.	

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

FT	DISULFID	53	143	BI SIMILARITY.
				BY SIMILARITY

FT	DISULFID	53	143
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P2A_MOUSE STANDARD; PRT; 146 AA.
 P31482; Q60871;
 01-JUL-1993 (Rel. 26, Created)
 01-FEB-1995 (Rel. 31, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 phospholipase A2, membrane associated precursor (EC 3.1.1.4)
 (phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
 (GLIC_SPUA2) (Enhancing factor) (EF).
 P1A2G2A.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=BALB/c;
 Mulherkar R.;
 Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 STRAIN=BALB/c; TISSUE=Intestine;
 MEDLINE=95403435; PubMed=7673223;
 Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
 A ywan M., Tang C., Rancourt D.E., Cromlish W.,
 "A natural disruption of the secretory group II phospholipase A2 gene
 in inbred mouse strains.";
 J. Biol. Chem. 270:22378-22385(1995).
 [3]
 SEQUENCE OF 22-146 FROM N.A.
 STRAIN=BALB/c; TISSUE=Small intestine;
 MEDLINE=94029955; PubMed=8267767;
 Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
 "Enhancing factor, a Paneth cell specific protein from mouse small
 intestines: predicted amino acid sequence from RT-PCR amplified cDNA
 and its expression.";
 Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
 [4]
 ERRATUM.
 MEDLINE=94071967; PubMed=8250944;
 Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
 Biochem. Biophys. Res. Commun. 197:351-352(1993).
 [5]
 SEQUENCE OF 29-146 FROM N.A.
 STRAIN=C3H;
 MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K.,
 Siracusa L.D., Buchberg A.M.;
 Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 [6]
 PRELIMINARY SEQUENCE OF 22-41.
 TISSUE=Small intestine;
 MEDLINE=93146172; PubMed=8425615;
 Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;
 "Enhancing factor protein from mouse small intestines belongs to the
 phospholipase A2 family.";
 FEBS Lett. 317:263-266(1993).
 -1- FUNCTION: MAY PLAY A ROLE IN CELL PROLIFERATION, BY INCREASING THE
 BINDING OF EGF TO THE CELLS AND THEREBY MODULATING ITS ACTION. IN
 DOING SO, THIS ISOZYME BINDS TO A MEMBRANE-ASSOCIATED RECEPTOR
 DISTINCT FROM THE EGF RECEPTOR AND WHICH COULD BE A HEPARAN-
 SULFATE PROTEOGLYCAN LOCATED ON THE CELL MEMBRANE.
 -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a fatty acid anion.
 -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 -1- SUBCELLULAR LOCATION: Membrane-associated.
 -1- TISSUE SPECIFICITY: MAINLY IN THE PANETH CELLS ADJACENT TO THE
 STEM POPULATION IN THE SMALL INTESTINES. ALSO EXPRESSED IN
 REGENERATING LIVER AND HYPERPLASTIC OEESOPHAGEAL EPITHELIUM.
 -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.

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OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:28 ; Search time 31 Seconds
(without alignments)
1116.642 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	402	42.0	69	4 Q9H415	Q9H415 homo sapien
2	319.5	33.4	138	13 Q90177	Q90177 trimeresuru
3	295.5	30.9	137	13 Q8UV08	Q8UV08 bothriechis
4	294.5	30.8	122	13 Q42187	Q42187 agkistrodon
5	290.5	30.4	138	13 Q91968	Q91968 trimeresuru
6	290	30.3	154	11 Q90X68	Q90X68 mesocricetu
7	287.5	30.0	146	11 Q91Y34	Q91Y34 rattus norv
8	284.5	29.7	122	13 Q42188	Q42188 agkistrodon
9	280.5	29.3	138	13 Q90W39	Q90W39 trimeresuru
10	277.5	29.0	138	13 Q90Z29	Q90Z29 echis color
11	269	28.1	138	13 Q92147	Q92147 trimeresuru
12	267.5	28.0	138	13 Q90395	Q90395 crotalus sc
13	263.5	27.5	138	13 Q8UV26	Q8UV26 crotalus at
14	263	27.5	122	13 Q42192	Q42192 agkistrodon
15	262.5	27.4	137	13 Q8UV27	Q8UV27 crotalus at
16	261.5	27.3	137	13 Q8UV07	Q8UV07 cerrophidio

17	258.5	27.0	137	13 Q92152	Q92152 trimeresuru
18	258	27.0	138	13 Q9PVF3	Q9PVF3 agkistrodon
19	251.5	26.3	122	13 Q91521	Q91521 vipera ammo
20	250.5	26.2	124	13 Q42190	Q42190 agkistrodon
21	249	26.0	137	13 Q91967	Q91967 vipera ammo
22	249	26.0	138	13 Q92118	Q92118 trimeresuru
23	247.5	25.9	119	13 Q91AT9	Q91AT9 bothriechis
24	245	25.6	124	13 Q42189	Q42189 agkistrodon
25	243.5	25.4	138	13 Q9PWR6	Q9PWR6 vipera pala
26	243.5	25.4	138	13 Q8UV25	Q8UV25 agkistrodon
27	242.5	25.3	138	13 Q57385	Q57385 agkistrodon
28	242.5	25.3	138	13 Q80G87	Q80G87 bothriechis
29	241.5	25.2	137	13 Q9PVF4	Q9PVF4 agkistrodon
30	240	25.1	139	13 Q9PVF2	Q9PVF2 agkistrodon
31	235	24.6	122	13 Q91506	Q91506 trimeresuru
32	233.5	24.4	138	13 Q910A0	Q910A0 echis color
33	232.5	24.3	138	13 Q910A1	Q910A1 vipera ammo
34	232	24.2	139	13 Q9PVE9	Q9PVE9 agkistrodon
35	228.5	23.9	122	13 Q918F8	Q918F8 bothriechis
36	227.5	23.8	139	13 Q92151	Q92151 trimeresuru
37	224	23.4	137	13 P79836	P79836 trimeresuru
38	221	23.1	126	13 Q9PVF1	Q9PVF1 agkistrodon
39	220	23.0	137	13 Q9YGJ7	Q9YGJ7 vipera pala
40	218	22.8	126	13 Q9PVF0	Q9PVF0 agkistrodon
41	218	22.8	149	13 Q9YH62	Q9YH62 dicentrarch
42	210	21.9	145	13 Q9DF52	Q9DF52 bungarus ca
43	210	21.9	152	13 Q8UW31	Q8UW31 lapemis har
44	206.5	21.6	145	13 Q90WA8	Q90WA8 bungarus fa
45	206.5	21.6	145	13 Q90WA7	Q90WA7 bungarus fa

ALIGNMENTS

RESULT 1
Q9H415
ID Q9H415 PRELIMINARY; PRT; 69 AA.
AC Q9H415;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DJ340N1.1 (Novel phospholipase similar to mouse phospholipase A2 group
DE IIF (PLA2G2F) (Fragment).
GN DJ340N1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z98257; CAC12707.1; -;
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
FT NON_TER 1
SQ SEQUENCE 69 AA; 7828 MW; D8CA44FC93040ED7 CRC64;

Query Match 42.0%; Score 402; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 DLNKTCEKQKTCMCDKNVLCMNQTYREYRGFLNVYCGPTPNCISYEPPEVTCSH 159
1 DLNKTCEKQKTCMCDKNVLCMNQTYREYRGFLNVYCGPTPNCISYEPPEVTCSH 60

QY 160 QSPAPPAPP 168
1 QSPAPPAPP 69

Db 61 QSPAPPAPP 69

RESULT 2

Mon Feb 10 11:36:19 2003

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Q90Y77      PRELIMINARY;          PRT;    138 AA.
ID Q90Y77;
AC Q90Y77;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A2 isoenzyme PL-Y.
DN
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN
RP
RQ
SEQUENCE FROM N.A.
RA Chifuwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
RA Nakashima K., Oda-Ueda N., Shimohigashi Y., Fukumaki Y., Hattori S.,
RA Ohno M.;
RT "Regional evolution of Trimeresurus flavoviridis venom-gland
RT phospholipase A2 isozymes."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072173; BAB68546.1; -
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip.1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN.1.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN.1.
DR SEQUENCE 138 AA; 15729 MW; C96B1E878CCAL196 CRC64;
SQ
Query Match 33.4%; Score 319.5; DB 13; Length 138;
Best Local Similarity 40.1%; Pred. No. 1.7e-27;
Matches 59; Conservative 28; Mismatches 49; Indels 11; Gaps 5;
QY 1 MKKFFTVAILAGSVLSTAHGSLNKLKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEV 60
Db 1 MRTLWIMAVL---LVGVEGHLQFRXMKIKMTGKEIPVSYAFYGYCGYCGRGRKPKDAT 56
QY 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIEVCSDLNKTCDKQTCMCDKNVLC 120
Db 57 DRCCFVHDCCEYK--TGCNPLTDTRYSHSLNKT-IVGGE-NK-PCLKEMCECDKAAIAC 111
QY 121 LMN--QTYREYRGFLNYVCOGPTNC 145
Db 112 FRDLNLTYYKKRYMTFPDICTDPTKEC 138
RESULT 3
Q8UVU8      PRELIMINARY;          PRT;    137 AA.
ID Q8UVU8;
AC Q8UVU8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Lys-49 phospholipase A2-like protein.
OS Bothriechis schlegelii (Eyelash palm pitviper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothriechis.
OX NCBI_TaxID=44725;
RN
RP
RQ
SEQUENCE FROM N.A.
RA Arch. Biochem. Biophys. 394:236-244(2001).
RA MEDLINE=21478653; PubMed=11594738;
RA Tsai I.H., Chen Y.H., Wang Y.M., Tu M.C., Tu A.T.;
RA "Purification, Sequencing, and Phylogenetic Analyses of Novel Lys-49
RT phospholipases A(2) from the Venoms of Rattlesnakes and other Pit
RT Vipers."
RL EMBL; AF374236; AAL39065.1; -
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip.1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
QY 121 LMN--QTYREYRGFLNYVCOGPTNC 145
Db 112 FRDLNLTYYKKRYMTFPDICTDPTKEC 138
RESULT 4
Q42187      PRELIMINARY;          PRT;    122 AA.
ID Q42187;
AC Q42187;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A2 (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN
RP
RQ
SEQUENCE FROM N.A.
RA Pan H., Wu X.F., Ouyang L.L., Liu X.L., Yang G.Z.;
RA "cDNA of phospholipase A2 from Agkistrodon halys Pallas."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015242; AAB71844.1; -
DR HSSP; P51972; 1VAP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip.1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR NON_TER 1
FT NON_TER 1
SQ
Query Match 30.8%; Score 294.5; DB 13; Length 122;
Best Local Similarity 40.9%; Pred. No. 8.5e-25;
Matches 52; Conservative 23; Mismatches 45; Indels 7; Gaps 4;
QY 21 SLLNKLKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEVDMCCHAHDCCYQELFDQCH 80
Db 1 SLLQFRKMKIKMTGKEIPVSYAFYGYCGYCGRGRKPKDATDRCCFVHDCCEYK--TGCN 58
QY 81 PVDYDHTIENNTIEVCSDLNKTCDKQTCMCDKNVLCMLN--QTYREYRGFLNYV 138
Db 59 PKWDDYTSWKNGT-IVCG--GDPCCKREVCECDKAAIACFRDLNLTYYKKRYMTYPNLC 115
QY 139 QGPTPNC 145
Db 116 SSKSEK 122
RESULT 5
Q9I968      PRELIMINARY;          PRT;    138 AA.
ID Q9I968;
AC Q9I968;

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DR	SWART; SHW0085; PA2c; 1.
DR	PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
DR	PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
KW	Hydrolase; Signal.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 154 SRC-ASSOCIATED PHOSPHOLIPASE A2.
SO	SEQUENCE 154 AA; 17217 MW; F5E0A76CE441772C CRC64;
 Query Match 30.3%; Score 290; DB 11; Length 154; Best Local Similarity 44.2%; Pred. No. 3.5e-24; Matches 57; Conservative 17; Mismatches 51; Indels 4; Gaps	
Qy	20 GSLLNLKAMVEAVTGRSAILSVFVGYGCGYGLGGRGPKDEVWCCHAHDCCYOELFPDQC 79 : : : : : : : : : : : :
Dd	21 GSLAEALNMIQLTMAGLSYAFYGCHGCLGGSGSPKDATTMCCAAHDCCYORLELGC 80 : : : : : : : : : : : : :
Qy	80 HPYYVDHYDHTIENNTETVCSDLNKTCDKQTCTCMCKNNVLCLM--NOTYREEYRGEFLNVY 137 : : : : : : : : : : : : : :
Dd	81 GTKSLEDNYFYSRG-EITCS-VNODFCQQQLCHCDRLLAECIAHQHSYSWKYLMDGIKK 138 : : : : : : : : : : : : : :
Qy	138 CGQTPNCS 146 : : :
Dd	139 CEGESPCS 147 : : :
 RESULT 7 Q91Y34 PRELIMINARY; PRT; 146 AA. AC Q91Y34 AC Q91Y34 DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Platelet phospholipase A2 precursor (Fragment). OS Rattus norvegicus (Rat). OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus; NCBI_TaxID=10116; [1] RN RATTUS NORVEGICUS FROM N.A. RC STRATIN-WISTAR; TISSUE=BLOOD; RA Lio T.T., Liang N.S., Meng Z.O., Xie Y.A., Kuang Z.P., Li Y.; RT "Cloning and sequence determination of rat platelet phospholipase A2 from whole blood." RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL: AF365363; AAK52061.1; - DR InterPro: IPR001211; PhospholipaseA2. DR Pfam: PF00068; phoslip.1. DR PRODOM: PD000303; PhospholipaseA2; 1. DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1. DR DR PROSITE; PS00118; PA2_HIS; UNKNOWN_1. KW Signal. FT SIGNAL 1 21 POTENTIAL. FT CHAIN 22 >146 PLATELET PHOSPHOLIPASE A2. FT NON_TER 146 146 SQ SEQUENCE 146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;	
 Query Match 30.0%; Score 287.5; DB 11; Length 146; Best Local Similarity 41.5%; Pred. No. 6.2e-24; Matches 59; Conservative 19; Mismatches 57; Indels 7; Gaps	
Qy	7 VALIA-GSVLSTAHGSLNLKAMVEAVTGRSAILSVFVGYGCGYGLGGRGPKDEVWCCH 65 : : : : : : : : : : : :
Dd	9 VVIWAFGSII-QVGSGELLEFGQMIPFKTGRRADVSFGYCHGVGGRGSPKDATMWCV 66 : : : : : : : : : : : : :
Qy	66 AHGCCYELEFDQGCHPYVDHYDHDTIENNTEIVGSIDLNKTCEDTKQTCMCNNMYLCML--N 123 : : : : : : : : : : : : :
Dd	67 THDCCYNLRKEKGCGTKELYKFYSYRGG-RISCS-TNQDSCRQLQCCDKAAACEFARNK 124 : : : : : : : : : : : : :
Qy	124 OTYREEYRGFNLVYCQGPPTNC 145 : : : : : : : : : : : : : :
Dd	125 KSYSLKYQFYFNKFCRKGTPTSC 146 : : : : : : : : : : : : : :

DE acylhydrolase (Lecithinase A) (PHOSPHATIDASE) (PHOSPHATIDOLIPASE).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Ogawa T.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93317604; PubMed=8327468;
 RA Nakashima K., Ogawa T., Oda N., Hattori M., Sakaki Y., Kihara H.,
 ONO M.;
 RT "Accelerated evolution of Trimeresurus flavoviridis venom gland
 phospholipase A2 isozymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5964-5968(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=94369106; PubMed=7765285;
 RA Nakashima K., Nobuhisa I., Ogawa T., Hattori M., Sakaki Y., Kihara H.,
 ONO M.;
 RT "Polymorphisms of Trimeresurus flavoviridis venom gland phospholipase
 A2 isozyme genes.";
 RL Biosci. Biotechnol. Biochem. 58:1510-1511(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95296360; PubMed=7777556;
 RA Nakashima K., Nobuhisa I., Deshimaru M., Nakai M., Ogawa T.,
 Shimohigashi Y., Fukumaki Y., Hattori M., Sakaki Y., Hattori S.,
 ONO M.;
 RT "Accelerated evolution in the protein-coding regions is universal in
 crotalinae snake venom gland phospholipase A2 isozyme genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5605-5609(1995).
 CC -/- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-
 ACYLGLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -/- COFACTOR: CALCIUM.
 DR EMBL: D10725; BAA01568.1; -;
 DR EMBL: D10723; BAA01566.1; -;
 DR HSSP: P14418; 1BK9.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF000068; phoslip; 1.
 DR PRINTS: PR00389; PHPLIPASEA2.
 DR PRODOM: PD000303; PhospholipaseA2; 1.
 DR SMART: SM00085; PA2c; 1.
 DR PROSITE: PS00119; PA2_ASP; 1.
 DR PROSITE: PS00118; PA2_HIS; 1.
 KW Signal.
 FT SIGNAL. 1 16 POTENTIAL.
 FT CHAIN 17 138 PHOSPHOLIPASE A2.
 FT SEQUENCE 138 AA; 15708 MW; AAD7DC04A6EDA975 CRC64;
 SQ SEQUENCE 138 AA; 15708 MW; AAD7DC04A6EDA975 CRC64;
 Query Match 28.1%; Score 269; DB 13; Length 138;
 Best Local Similarity 37.7%; Pred. No. 6.5e-22;
 Matches 57; Conservative 21; Mismatches 59; Indels 14; Gaps 5;
 QY 1 MKKFTTAVILAGSVLSTAGHSLNLKAMVEAVTGRSAILSFVGYGCGGLGRGPKDEV 60
 Db 1 MRLTWIMAVL----LVGVGSLVFEFETLIMKTAGRSIGSYSSYSGYCGAGGQWPQDS 56
 QY 61 DMCCHAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 Db 57 DRCCFVHDCCYGVK--TGCDPKDDFYIYSSENG-DIVCGD--DDLCKKVECDKRAAIC 111
 QY 121 LMNQTREERYRGFLNVCYCGTPTNCPNC 145
 Db 112 FRDSMNTYDYKYLRFSPENCQGESQPC 138
 RESULT 13
 Q8UVZ6 PRELIMINARY; PRT; 138 AA.
 ID Q8UVZ6 PRELIMINARY; PRT; 138 AA.
 AC Q8UVZ6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acidic phospholipase A2 precursor.
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.;
 RT "Cloning, characterization and phylogeny of two novel Lys-49
 phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom
 glands.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RESULT 12
 Q90395 PRELIMINARY; PRT; 138 AA.
 ID Q90395
 AC Q90395;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Preproacidic subunit of mojave toxin precursor.
 OS Crotalus scutulatus scutulatus (Mojave rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8738;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=94156205; PubMed=8112610;
 RA John T.R., Smith L.A., Kaiser I.I.;
 RT "Genomic sequences encoding the acidic and basic subunits of Mojave
 toxin; unusually high sequence identity of non-coding regions.";
 RL Gene 139:229-234(1994).
 DR EMBL: U01026; AAC59673.1; -;
 DR HSSP: P00624; 1PP2.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF000068; phoslip; 1.
 DR PRINTS: PR00389; PHPLIPASEA2.
 DR PRODOM: PD000303; PhospholipaseA2; 1.
 DR SMART: SM00085; PA2c; 1.
 DR PROSITE: PS00119; PA2_ASP; 1.
 DR PROSITE: PS00118; PA2_HIS; 1.
 KW Signal.
 FT SIGNAL. 1 16 POTENTIAL.
 FT CHAIN 17 138 PHOSPHOLIPASE A2.
 FT SEQUENCE 138 AA; 15211 MW; 8164C7C8D27D6EBE CRC64;
 SQ SEQUENCE 138 AA; 15211 MW; 8164C7C8D27D6EBE CRC64;
 Query Match 28.0%; Score 267.5; DB 13; Length 138;
 Best Local Similarity 38.8%; Pred. No. 9.6e-22;
 Matches 57; Conservative 18; Mismatches 61; Indels 11; Gaps 5;
 QY 1 MKKFTTAVILAGSVLSTAGHSLNLKAMVEAVTGRSAILSFVGYGCGGLGRGPKDEV 60
 Db 1 MRLTWIMAVL----LVGVGSLVFEFETLIMKTAGRSIGSYSSYSGYCGAGGQWPQDS 56
 QY 61 DMCCHAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 Db 57 DRCCFVHDCCYAKL--TGCDPTTDTYTRQEDG-EIVCG--GDDPCGTQICECDRAAIC 111
 QY 121 LMN--QTYREERYGFLNVCYCGTPTNCPNC 145
 Db 112 FRDSMNTYDYKYLRFSPENCQGESQPC 138
 RESULT 13
 Q8UVZ6 PRELIMINARY; PRT; 138 AA.
 ID Q8UVZ6 PRELIMINARY; PRT; 138 AA.
 AC Q8UVZ6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acidic phospholipase A2 precursor.
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.;
 RT "Cloning, characterization and phylogeny of two novel Lys-49
 phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom
 glands.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

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QY 141 PTPNCSIYEPP 151
   |  || .  |
Db 111 PARNCOESEP 121

RESULT 15
Q8UVZ7
ID Q8UVZ7 PRELIMINARY; PRT; 137 AA.
AC Q8UVZ7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lys-49 phospholipase A2 precursor.
OS Crotalus atrox (western diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
ON NCBI_TaxID=8730;
RX [1]
RN
RP SEQUENCE FROM N.A.
RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.;
RA "Cloning, characterization and phylogeny of two novel Lys-49
RT phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom
RT glands.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF269130; AAL36973.1; -
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF00068; phoslip; 1.
DR ProDom: PD000303; PhospholipaseA2; 1.
DR SMART: SM00085; PA2c; 1.
DR PROSITE: PS00119; PA2_ASP; UNKNOWN_1.
DR PROSITE: PS00118; PA2_HIS; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 1 16 POTENTIAL.
           17 137 LYS-49 PHOSPHOLIPASE A2.
           SEQUENCE 137 AA; 15597 MW; 63EF8D0D565AE6 CRC64;

Query Match      27.4%; Score 262.5; DB 13; Length 137;
Best Local Similarity 39.2%; Prd. No. 3.4e-21;
Matches 56; Conservative 27; Mismatches 49; Indels 11; Gaps

QY 1 MKKFFTVALLAGSVLSHTAGSLNLKAMVEAVGTGSAILSFVGYCYCGLGRGOPDEV 60
   | : : | | : | | | | : | : | : | : | : | | | | | | | | | |
Db 1 MTFFWIVAML----LVGVESLVELGKNIILOETGKNPTTSYGIYCGNGVSRRHKPKDGT 56

QY 61 DMCCHAHDCCYQLFDGCHPYVDHYDHTIENNTEITVCSDLNKTCDKOTCMCKDNMYLC 120
   | | | | : | | | : | : | : | : | : | : | : | : | : |
Db 57 DRCCFVHKCCYKKLTD--CDPKMDGYTYPFKDT-IIC-DVN-NPCLKEMCECDKAIVAIC 111

QY 121 LMN--QTYYEEYRFLNVYCGP 141
   | | | : | : | : | : | : |
Db 112 LRENLDTNKKIKYIFPLCKKP 134

Search completed: February 10, 2003, 10:37:09
Job time : 32 secs
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